! FINDPATTERNS on pir: \* allowing 0 mismatches

Databases searched: NBRF, Release 73.0, Released on 16Aug2002, Formatted on 20Aug2002 ses; x - any Ax

Total sequences
CPU time 96,134,422 283,224 01:02.36

reference & a light ment dat a are arrower sets for the issued, pending & A-Genesez files. The the Quest program provides the たっと、

of the dx scaring table. Finally, there are 2 disks Point of Contact

Technical Info. Specialist CM1 6B05 Tel: 305-4053

Susan Hanley

1 \*(A,D,E,F,G,I,N,S,V)[0,1](A,D,E,H,I,L,M,0,S)[0,1](D,E,F,H,N,M,P,V,M)[0,1](A,D,E,T)) Sear Che both the PIR & Swissport length (see le,ft). here were no the files were huge & unmanageable, then I searched exact length of the database sequence. ammen in Swissprot a pix for the sequences w/ no limitations on 'databases. Atfirst, I searched the GCG program, find patterns, Ex. patterson,

anamo wer sets for each class a base the seg 2 swpl. find (a) seg 2 pirl. find) file shows the align ments & the accession number of the database seg. The oret mary them together.) accession number, (Sorry I can't tiles give the internation or the the exact length se then I served the sequence

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any AA 1-20 time

FIND ATTERNS on swp: \* allowing 0 mismatches \$1 <x(0,20)(A,D,E,F,G,I,N,S,V)(0,1)(A,D,E,H,I,I,M,0,S)(0,1)(D,E,F,H,N,M,P,V,W)(q,1)(A,D,E,T)DRX {1,20}} = and of
any of these oil times

al20\_CARMA ck: 9046 lbn. c. Endpatterno runo

FIBB\_LAMGL FIBB\_FELCA FIBB\_BUBBU FIBB\_BISBO FIBB\_CEREL FIBB\_ANTAM DNIV\_BPD10 AMD1\_RABIT AMD1\_CHICK <u>ب</u> <u>..</u> 1: <u>..</u> -: ۲. <u>ب</u> <u>..</u> 1: ck: 4317 len: 19 ck: 5816 len: 20 ck: 6821 len: 21 ck: 7185 len: 21 ck: 7213 len: 21 ck: 7016 len: 21 ck: 9004 len: 22 ck: 7826 len: 26 ck: 7006 len: 26 <X[0,20](A,D,E,F,G,I,N,S,V)[0,1](A,D,E,H,I,L,M,Q,S)[0,1](D,E,F,H,X[9](E)DRX[8]
IIDYYDEGEEDRDVGVVDAR</pre> <X[0,20](A,D,E,F,G,I,N,S,V)[0,1](A,D,E,H,I,L,M,Q,S)[0,1](D,E,F,H,X[10](E)DRX[8]
QHSTDYDEEEEDRAKLHLDAR</pre>  $\begin{array}{l} \langle x\{0,20\}\{A,D,E,F,G,I,N,S,V\}\{0,1\}\{A,D,E,H,I,L,M,Q,S\}\{0,1\}\{D,E,F,H,x\{10\}\{D\}DRx\{\theta\}\\ QFPTDYDEGQDDRPKLGLGAR \end{array}$ <X{0,20}{A,D,E,F,G,I,N,S,V}{0,1}{A,D,E,H,I,L,M,Q,S}{0,1}{D,E,F,H,
x{10}{D}DRx{8}
EFPTDYDEGEDDRPKVGLGAR</pre> <X{0,20}(A,D,E,F,G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,H,X{10}(D)DRX{8})
QPSYDYDEEEDDRAKLRLDAR</pre> <X{0,20}{A,D,E,F,G,I,N,S,V}{0,1}{A,D,E,H,I,L,M,Q,S}{0,1}{D,E,F,H, x{5}{E}DRx{18} GYEDEDEDRFYALGLGKRPRTYSFGL <X{0,20}(A,D,E,F,G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,H
x{13}(D)DRx{6}
YKKHPAKRTHIENDDRINQIDR</pre> <X[0,20](A,D,E,F,G,I,N,S,V)[0,1](A,D,E,H,I,L,M,Q,S)[0,1](D,E,F,H,X[16](A)DRX[6]
MNQKHLLRFIKKSYQVDADRVVYSTK</pre> <X{0,20}(A,D,E,F,G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,H,X{16}(A)DRX{6}
MNQKHLLRFIKKSYRVDADRVVYDAK</pre> ! P14473 lama glama (llama), lama vicugna (v ! P14469 felis silvestris catus (cat). fibri ! P14468 cervus elaphus (red deer), and ! P14467 bubalus bubalis (domestic water buf ! P14466 bison bonasus (european bison). fib ! P14465 antilocapra americana (pronghorn). ! Q38199 bacteriophage d108. dna-invertase (1 ! P81073 gallus gallus (chicken). amp deamina ! P81072 oryctolagus cuniculus (rabbit). amp

FIBB\_RANTA ck: 6866 len: 21 ! P14479 rangifer tarandus (reindeer) (car <x{0,20}(A,D,E,F,G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F, x{10}(D)Dkx{8} QHLADYDEVEDDRAKLHLDAR

GLU1\_ORENI ck: 382 len: 36 ! P81026 oreochromis niloticus (nile tilap <\( \)(0,20\)(A,D,E,F,G,I,N,S,V)\( \)(0,1\)(A,D,E,H,I,L,M,Q,S)\( \)(0,1\)(D,E,F,X\)(14\)(B)DRX\( \)(19\)
1: HSEGTFSNDYSKYLEDRKAQDFVRWLMNNKRSGAAE

MY14\_EISFO ck: 7600 len: 14 ! P46979 eisenia foetida (common brandling <X[0,20](A,D,E,F,G,I,N,S,V)[0,1](A,D,E,H,I,L,M,Q,S)[0,1](D,E,F,X {5}(A)DRX {5} GFKDGAADRISHGF

Q9ZG33 ck: 1658 len: 17 ! Q9zg33 chlamydia trachomatis. subtilisin

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CX(0.20)(A.D.E.F.G.I.N.S.Y)(0.1](A.D.E.H.I.L.M.Q.S)[0.1](D.E.F.H.N. X18)(T)DER(S)  WEGOPETDERNSERI  Q9XIL6 Ck: 2042 len: 24   Q9Xil6 streptomyces coelicolor a3(2). f81r  CX(0.20)(A.D.E.F.G.I.N.S.Y)(0.1](A.D.E.H.I.L.M.Q.S)[0.1](D.E.F.H.N. X1A)(A)DEX(19)  AX(A)(A)DEX(19)  MADRECTDEATAGRAGSRAPEF  Q9X9U4 Ck: 4039 len: 25   Q9X9U4 streptomyces coelicolor. adp glucosed  CX(0.20)(A.D.E.F.G.I.N.S.Y)(0.1](A.D.E.H.I.L.M.Q.S)[0.1](D.E.F.H.N. X119)(A)DEX(4)  MIGHYLAGGRAGHAPHIADRAKPA  Q49137 Ck: 9647 len: 32   Q49137 methylobacterium extorquens. mxas pri CX(0.20)(A.D.E.F.G.I.N.S.Y)(0.1](A.D.E.H.I.L.M.Q.S)[0.1](D.E.F.H.N. X111)(A)DEX(13]  ALRHICAPPAREPERLADREDARLISHHAMT  Q5914 Ck: 3366 len: 9   Q59314 streptomyces cyaneus (streptomyces cyaneus (cyaneus (cyaneus cyaneus (cyaneus cyaneus											
X(0,20)(A,D,E,F,G,I,N,S,V)(0,1)(A,D,E,H,I,L,M,Q,S)(0,1)(D,E,F,H,N,X(B)(F)DBX(S))  Ck: 2042 len: 24   O9kil6 streptomyces coelicolor a3(2), f8lr  X(1)(A)DBX(19)  KADDETCTDERABERALGSRAPEE  Ck: 4039 len: 25   O9x9u4 streptomyces coelicolor. adp glucose  Ck: 4039 len: 25   O9x9u4 streptomyces coelicolor. adp glucose  Ck: 4039 len: 22   O49137 methylobacterium extorquens. mxas pr  X(10,20)(A,D,E,F,G,I,N,S,V)(0,1)(A,D,E,H,I,L,M,Q,S)(0,1)(D,E,F,H,N,1)(1)(A,D,E,F,G,I,N,S,V)(0,1)(A,D,E,H,I,L,M,Q,S)(0,1)(D,E,F,H,N,1)(1)(D,E,F,H,N,	Q99094	Q03977 1:	Q93A08 1:	ف	0542	L D	(in	Q49137 1:	Q9X9U4 1:	1: Q9KIL6 1:	
	1642 len: 36 ! Q99094 salmonella typhimurium. mkaa 0,20}(A,D,E,F,G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D, {15}(D)DKx{18}	<pre>ck: 4923 len: 19 ! Q03977 escherichia coli. alpha-acceptor pol <x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n mtmitdslavvartdrpsq<="" pre="" x{13}{t)drx{3}=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n></pre>	5753 len: 12 ! Q93a08 thiobacillus ferrooxidans. resb 0,20}(A,D,E,E,G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,E [2](Q)(D)DRx(6) SQDDRKENNDG	9419 len: 22 0,20}(A,D,E,F,G, (9)(D)DRx{10} QNFINPDLDDRTEKDL	6757 len: 38 . O05422 mycobacterium marinum. phytoene 0,20](A,D,E,F,G,I,N,S,V)[0,1](A,D,E,H,I,L,M,Q,S)[0,1](D,E,E) (15](A)DEx{19] PGYGVPTTLISGRLAADRITGNTTRSIRHLDLKAQLS	7152 len: 13   Q50476 mycobacterium tuberculosis. c 0,20}(A,D,E,F,G,I,N,S,V)[0,1](A,D,E,H,I,L,M,Q,S)[0,1](D, {8)(T)DRx(2) PEQHPPITDRSR	) ! Q53914 streptomyces cyaneus (streptomy	9647 len: 32 ! Q49137 methylobacterium extorquens. mxas 0,20}(A,D,E,F,G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,H (16)(A)DEX{13} LRRICAPFARPPFRLADRFDAEALSRHLMTT	4039 len: 25 ! Q9x9u4 streptomyces coelicolor. adp 0,20](A,D,E,F,G,I,N,S,V)[0,1](A,D,E,H,I,L,M,Q,S)[0,1](D, [18](A)DEX{4} LGIVLAGGEGKRLMPLTADRAKPA	<pre>FLGQPFCTDRKNSFRI  2042 len: 24 ! Q9ki16 streptomyces coelicolor a3(2).  20,20, A, D, E, F, G, I, N, S, V) {0,1} (A, D, E, H, I, L, M, Q, S) {0,1} (D, E, A) (A) (D) DX {19}  ADDRTGTDEATAERALGSRAPEF</pre>	<x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n< td=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n<>

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1: GSQDFASQLSKLRLSDDRTADTNRIKRIINMRYLNS

Q9NZ25 ck: 6136 len: 20 ! Q9nZ25 homo sapiens (human). atp7b (frag

<x{0,20}(A,D,E,F,G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,X{6}(A)DRX{11}

x{6}(A)DRX{11}
APIQQLADRFSGYFVPFIVI

Q9UCI1 ck: 8961 len: 15 ! Q9uci1 homo sapiens (human). tropomyosin <x{0,20}{A,D,E,F,G,I,N,S,V}{0,1}{A,D,E,H,I,L,M,Q,S}{0,1}{D,E,F,x{2}(E)(A)DRx{7}} l:

Q96F68 ck: 588 len: 28 ! Q96f68 homo sapiens (human). unknown (pr <x(0,20)(A,D,E,F,G,I,N,S,V)[0,1](A,D,E,H,I,L,M,Q,S)[0,1](D,E,F,x(10)(A)DRx(15) vsQpGSCRHGADRVGHVGQRAGAGVRPE

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1 062575 tetracapsula bryozoides. hox protein composition of the compo	ck: 7242 len: 20 <x{0,20}(a,d,e,f)< th=""><th>062575</th></x{0,20}(a,d,e,f)<>	062575
ck: 8106 len: 21 ! Q9twrl bombyx mori (silk moth). cysteine pr <x[0,20](a,d,e,f,g,i,n,s,v)[0,1](a,d,e,h,i,l,m,q,s)[0,1](d,e,f,h,n x[5](D)DRX[13] XPEQVDDRKHGAVTDDKXXQX</x[0,20](a,d,e,f,g,i,n,s,v)[0,1](a,d,e,h,i,l,m,q,s)[0,1](d,e,f,h,n 	ck: 8106 len: 21 <x{0,20}(a,d,e,f, td="" xpeqvddrkhgavtd<="" x{5}(d)drx{13}=""><td>Q9TWR1</td></x{0,20}(a,d,e,f,>	Q9TWR1
<pre>! Q9v973 drosophila melanogaster (fruit fly). N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,H,N</pre>	ck: 1645 len: 17 <x[0,20](a.d.e.f.g.i. x[4](S)(T)DRX[9] мецsstdrgpннадодя</x[0,20](a.d.e.f.g.i. 	Q9V973 1:
! O18615 artemia salina (brine shrimp). ftz-f G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,H,N DRSCHIDKSQRKRCPPCRF	ck: 5276 len: 34 <x{0,20}(a,d,e,f, fkrtyqnkkyytcma<="" td="" x{14}(a)drx{17}=""><td>018615 1:</td></x{0,20}(a,d,e,f,>	018615 1:
7 ! 002602 beroe ovata. homeobox protein bhox35 ',G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,H,N SRGVNLTDRQVKI	ck: 9552 len: 27 ! 002602 <x[0,20](a,d,e,f,g,i,n,s,v)[0 x[20](T)DRx[4] LFNMYLTRERRLEISRGVNLTDRQVKI</x[0,20](a,d,e,f,g,i,n,s,v)[0 	002602
beroe ovata. homeobox protein bhox26,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,H,N	ck: 9410 len: 27 ! p91901 <x[0,20](a,d,e,f,g,i,n,s,v)[0 lfnmyltrerrleisksinltdrqvki<="" td="" x[20](t)dbx{4]=""><td>P91901 1:</td></x[0,20](a,d,e,f,g,i,n,s,v)[0>	P91901 1:
<pre>sacculina carcini. caudal (fragment) ,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,H,N</pre>	<pre>ck: 9212 len: 27 ! 096892 <x{0,20}{a,d,e,f,g,i,n,s,v}{0} pre="" rfnnyitikrklelsrilgltdrqvki<="" x{20}{t}drx{4}=""></x{0,20}{a,d,e,f,g,i,n,s,v}{0}></pre>	096892
<pre>chaetopterus variopedatus. chv-hbl1 ,1)(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,H,N)</pre>	ck: 8578 len: 27 ! Q94458 <x{0,20}{a,d,e,f,g,i,n,s,v}{0 x{20}{D}DRX{4} NQKKFIEKKDRDRISNEIGLDDRQIKY</x{0,20}{a,d,e,f,g,i,n,s,v}{0 	Q94458 1:
<pre>metridium senile (brown sea anemone) ,1)(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,H,N)</pre>	ck: 9269 len: 27 ! Q25482 <x[0,20](a,d,e,f,g,i,n,s,v){0 x{20](T)DRx{4} HFNHFLTKERRSEMATQLNLTDRQVKI</x[0,20](a,d,e,f,g,i,n,s,v){0 	Q25482 1:
<pre>ctenodrilus serratus. ovxl ortholog ,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,H,N)</pre>	ck: 8475 len: 27 ! Q23749 <x{0,20}{a,d,e,e,g,i,n,s,v}{0} x{19}{T}DRX{5} PQQEILVTDGTIAHRASPETDRGSGEN</x{0,20}{a,d,e,e,g,i,n,s,v}{0} 	Q23749 1:
<pre>81 polyandrocarpa misakiensis. pmhbox1 {0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,H,N</pre>	ck: 5282 len: 25 ! Q946 <x[0,20](a,d,e,f,g,i,n,s,v) x[20](T)DRX[2] HFNQYLCRERRQEVAKAVNLTDRQV</x[0,20](a,d,e,f,g,i,n,s,v) 	Q94681 1:

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                                                                                                                                                                                                                                               Q61676
                                                                                          8MZM60
                                                                                          ck: 2931 len:
                                                                                                                                                                                                                                                 ck: 8698 len: 27
<X[0,20](A,D,E,F,G,I,N,S,V)[0,1](A,D,E,H,I,L,M,Q,S)[0,1](D,E,F,
x[18](D)DRx[7]
GRDCQDHSFSIVIETVQCADDRDAVCTRS</pre>
                                                                                                                                                    <X[0,20](A,D,E,F,G,I,N,S,V)[0,1](A,D,E,H,I,L,M,Q,S)[0,1](D,E,F,
x[8](A)DRX[16] .
LYQKYLSPADRDEIAASLGLSNAQVIT</pre>
                                                                                                                                                                                                                                                                                                                x{20}(T)DRx{3}
LENMYLSRERRLEISKSIDLTDRQVK
                                                                                                                                                                                                                                            ! Q61676 drosophila melanogaster (fruit fl
                                                                                     ! Q9mzw8 pongo pygmaeus (orangutan). von w
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<del>..</del> <u>..</u> Q9TRS7 ck: 2610 len: 24 <X{0,20}(A,D,E,F,G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,
x{14}(A)DRx{7}
AQESXKGRVTEGFNADRKQQQDEL</pre> <X{0,20}(A,D,E,F,G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,
x{10}(T)DRx{9}
DDLDEKTEGSDTDRLLSNDHEKS</pre> ! Q9trs7 canis familiaris (dog). vitronect

029394

ck: 807

len: 23

! Q29394 canis familiaris (dog). growth ho

1. Q9TQQ9ck: 8644 len: 15 <X[0,20](A,D,E,F,G,I,N,S,V)[0,1](A,D,E,H,I,L,M,Q,S)[0,1](D,E,F,
x{2}(A)(A)(A)DRx{8}
EEAAADREDDPNFFK</pre> ! Q9tqq9 bos taurus (bovine). glutamate de

<u>..</u> Q9TR40 ck: 8661 len: 15 <x{0,20}(A,D,E,F,G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,
x{2}(A)(A)(A)DRx{8}
VEAAADREDDPNFFK</pre> 1 Q9tr40 bos taurus (bovine). glutamate de

<u>..</u> Q9TRF2 ck: 1454 len: 33 <X{0,20}(A,D,E,F,G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,
x{17}(D)DRx{13}
XVNVDKYLERDQKLSELDDRADALQAGASQFET</pre> ! Q9trf2 bos taurus (bovine). vamp/synapto

Q37112 ck: 9119 len: <x{0,20}(A,D,E,F,G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,x{5}{T})DRx{14}
MEYLTTDRSIECGIYLKKIESI</pre> 22 ! Q37112 pinus thunbergii (green pine) (ja

1:

Ξ. Q957T4 ck: 9875 len: 22 <X{0,20}(A,D,E,F,G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,
x{17}(T)DRx{2}
mpTSNQSIRHGREKKRRTDRTR</pre> ! Q957t4 abies alba (edeltanne) (european

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:: Q957T0ck: 1370 len: 23 <X{0,20}(A,D,E,F,G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,
x{17}(T)DRx{3}
mPTSNQSIRHGREKKRRTDRTRA</pre> ! Q957t0 pinus mugo. ribosomal protein s12

L	ck: 2605 len: 29 ! Q9s8d2 cucumis melo (muskmelon). cmeti-b=tr	Q9S8D2
	<pre><x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,o,s){0,1}(d,e,f,h,n,x(12)(t)drx(4) aianaplldttitdrvffd<="" pre=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,o,s){0,1}(d,e,f,h,n,x(12)(t)drx(4)></pre>	<b>:</b>
	9 ck: 4307 len: 19   P83089 spinacia oleracea (spinach). thylako	P83089
	<pre><x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x){6}(e)drx{20} pre="" xahtredrtarhvrirkkvegtperxxl<=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x){6}(e)drx{20}></pre>	1:
ı	6 ck: 4154 len: 29 ! P82196 spinacia oleracea (spinach). chlorop	P82196
	$ \begin{array}{l} <\mathbf{x}\{0,20\}(\mathtt{A},\mathtt{D},\mathtt{E},\mathtt{F},\mathtt{G},\mathtt{I},\mathtt{N},\mathtt{S},\mathtt{V})\{0,1\}(\mathtt{A},\mathtt{D},\mathtt{E},\mathtt{H},\mathtt{I},\mathtt{L},\mathtt{M},\mathtt{Q},\mathtt{S})\{0,1\}(\mathtt{D},\mathtt{E},\mathtt{F},\mathtt{H},\mathtt{N},\mathtt{X},\mathtt{G})\{\mathtt{D},\mathtt{D},\mathtt{R},\mathtt{A},\mathtt{I},\mathtt{I},\mathtt{M},\mathtt{Q},\mathtt{S},\mathtt{A},\mathtt{I},\mathtt{I},\mathtt{M},\mathtt{Q},\mathtt{S},\mathtt{A},\mathtt{I},\mathtt{I},\mathtt{M},\mathtt{Q},\mathtt{S},\mathtt{A},\mathtt{I},\mathtt{I},\mathtt{M},\mathtt{Q},\mathtt{S},\mathtt{A},\mathtt{M},\mathtt{M},\mathtt{M},\mathtt{M},\mathtt{M},\mathtt{M},\mathtt{M},M$	1:
<b>L</b> .1	5 ck: 7110 len: 26   P82195 spinacia oleracea (spinach). chlorop	P82195
	<pre><x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n ngsqadrsvgqklaphlnvrpsi<="" pre="" x(4)(a)drx{16}=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n></pre>	1:
<b>ں</b>	3 ck: 1444 len: 23 ! Q39633 cucumis sativus (cucumber). catalase	Q39633
	<pre><x[0,20](a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x){20}(e)drx[6] mddvddvfsyllskeideenedrepkyyy<="" pre=""></x[0,20](a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x){20}(e)drx[6]></pre>	<del>!</del>
L	4 ck: 3486 len: 29 ! Q9fzp4 arabidopsis thaliana (mouse-ear cres	Q9FZP4
	<pre><x{0,20}{a,d,e,f,g,i,n,s,v}{0,1}{a,d,e,h,i,l,m,q,s}{0,1}{d,e,f,h,n x{8}{TJDRx{17}} peiahmyktdrakyestarswtokyamg</x{0,20}{a,d,e,f,g,i,n,s,v}{0,1}{a,d,e,h,i,l,m,q,s}{0,1}{d,e,f,h,n </pre>	1:
Д	9 ck: 1580 len: 28 ! Q42209 arabidopsis thaliana (mouse-ear cres	Q42209
	<pre><x[0,20](a,d,e,f,g,i,n,s,v)[0,1](a,d,e,h,i,l,m,q,s)[0,1](d,e,f,h,n alrylalnedrkfrskhv<="" pre="" x[0](e)drx[7]=""></x[0,20](a,d,e,f,g,i,n,s,v)[0,1](a,d,e,h,i,l,m,q,s)[0,1](d,e,f,h,n></pre>	<b>1</b>
L	2 ck: 3123 len: 18 ! Q37852 bacteriophage r17. a protein (fragme	Q37852
	<pre><x{0,20}{a,d,e,f,g,i,n,s,v}{0,1}{a,d,e,h,i,l,m,q,s}{0,1}{d,e,f,h,n x{14}{A}DRx{7} ATVVAPKYTSIKPTADRVLIKIKE</x{0,20}{a,d,e,f,g,i,n,s,v}{0,1}{a,d,e,h,i,l,m,q,s}{0,1}{d,e,f,h,n </pre>	1:
	3 ck: 2853 len: 24 ! Q9t2h3 spinacia oleracea (spinach). chapero	09т2н3
	<pre><x(0,20)(a,d,e,f,g,i,n,s,v)(0,1)(a,d,e,h,i,l,m,q,s)(0,1)(d,e,f,h,n gsssladrlxlgslaxdgfs<="" pre="" x(3)(s)(l)(a)drx(12)=""></x(0,20)(a,d,e,f,g,i,n,s,v)(0,1)(a,d,e,h,i,l,m,q,s)(0,1)(d,e,f,h,n></pre>	<b>!</b> :
	6 ck: 5922 len: 20 ! Q9t2k6 cucurbita moschata (cushaw squash) (	Q9Т2К6
	<pre><x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x,t){t}){t}drx{3} mptsnqsirhgrekkrtdrtra<="" pre=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x,t){t}){t}drx{3}></pre>	1:
	8 ck: 1370 len: 23 ! Q957s8 pinus sylvestris (scots pine). ribos	Q957S8

1:			
VGCPRILMKCKTDRDCLTGCTCKRNGYCG	x{11}(T)DRx{15}	$(X_{0,20},A,D,E,F,G,I,N,S,V)_{0,1},A,D,E,H,I,L,M,Q,S)_{0,1}_{0,1}_{0,E,F}$	

- Q9QVF2 ck: 5863 len: 12 | Q9qvf2 rattus sp. transferrin=peptide 21 <X{0,20}(A,D,E,F,G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,X{5}(A)DRx!4} 1: NLANKADRDQYE

- Q63990 ck: 5506 len: 25 ! Q63990 rattus norvegicus (rat). hox3.5 h
  <X(0,20){A,D,E,F,G,I,N,S,V}{0,1}{A,D,E,H,I,L,M,Q,S}{0,1}{D,E,F,
  x{20}{T}DRx{2}
  LFNMYLTRERRLEISKTINLTDRQV
- O88226 ck: 2429 len: 33 ! O88226 mus musculus (mouse). mszf76 (fra <X[0,20](A,D,E,F,G,I,N,S,V)[0,1](A,D,E,H,I,L,M,Q,S)[0,1](D,E,F, x[17](T)DRX[13]

  1: IHTGEKPYRCAECGKAFTDRSNLIKHQTTHTGE
- Q9JIU0 ck: 1050 len: 32 ! Q9jiu0 rattus norvegicus (rat). protocad <\( \)(0,20)(A,D,E,F,G,I,N,S,V)(0,1)(A;D,E,H,I,L,M,Q,S)\( 0,1\)(D,E,F,\( \)(10)\( \)(T)\( \)DRX\( 18\) ALQAFEFHYGATDRGSPALSSQALVRVVVLDN
- Q9ET00 ck: 5807 len: 20 ! Q9et00 mus musculus (mouse). eif4h (frag <\x{0,20}\{A,D,E,F,G,I,N,S,V}\{0,1\}\((A,D,E,H,I,L,M,Q,S)\{0,1\}\((D,E,F,X^7)\)\((D,D,E,F,B,I,L,M,Q,S)\)\((D,D,E,F,B,I,L,M,Q,S)\)\((D,D,E,F,B,I,L,M,Q,S)\)\((D,D,E,F,B,I,L,M,Q,S)\)\((D,D,E,F,B,I,L,M,Q,S)\)\((D,D,E,F,B,I,L,M,Q,S)\)\((D,D,E,F,B,I,L,M,Q,S)\)\((D,D,E,F,B,I,L,M,Q,S)\)\((D,D,E,F,B,I,L,M,Q,S)\)\((D,D,E,F,B,I,L,M,Q,S)\)\((D,D,E,F,B,I,L,M,Q,S)\)\((D,D,E,F,B,I,L,M,Q,S)\)\((D,D,E,F,B,I,L,M,Q,S)\)\((D,D,E,F,B,I,L,M,Q,S)\)\((D,D,E,F,B,I,L,M,Q,S)\)\((D,D,E,F,B,I,L,M,Q,S)\)\((D,D,E,F,B,I,M,Q,S)\)\((D,D,E,F,B,I,M,Q,S)\)\((D,D,E,F,B,I,M,Q,S)\)\((D,D,E,F,B,I,M,Q,S)\)\((D,D,E,F,B,I,M,Q,S)\)\((D,D,E,F,B,I,M,Q,S)\)\((D,D,E,F,B,I,M,Q,S)\)\((D,D,E,F,B,I,M,Q,S)\)\((D,D,E,F,B,I,M,Q,S)\)\((D,D,E,F,B,I,M,Q,S)\)\((D,D,E,F,B,I,M,Q,S)\)\((D,D,E,F,B,I,M,Q,S)\)\((D,D,E,F,B,I,M,Q,S)\)\((D,D,E,F,B,I,M,Q,S)\)\((D,D,E,E,B,I,M,Q,S)\)\((D,D,E,E,B,I,M,Q,S)\)\((D,D,E,E,B,I,M,Q,S)\)\((D,D,E,E,B,I,M,Q,S)\)\((D,D,E,E,B,I,M,Q,S)\)\((D,D,E,E,B,I,M,Q,S)\)\((D,D,E,E,B,I,M,Q,S)\)\((D,D,E,E,B,I,M,Q,S)\)\((D,D,E,E,B,I,M,Q,S)\)\((D,D,E,E,E,B,I,M,Q,S)\)\((D,D,E,E,B,I,M,Q,S)\)\((D,D,E,E,B,I,M,Q,S)\)\((D,D,E,E,B,I,M,Q,S)\)\((D,E,E,E,B,I,M,Q,S)\)\((

**ب** 

Q9Z115 ck: 4927 len: 19 ! Q9Z115 rattus sp. calcineurin a alpha (e < X{0,20}(A,D,E,F,G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,X{13}{T})DRX{3}
1: MSEPKAIDPKLSTTDRVVK

Q66538 ck:	Q65747 ck: <x{c x{ 2H</x{c 		Q61461 ck:	1: cx{0	Q9QV71 ck:	-x{0 -x{ 1: EI	Q9QV89 ck:	1: <	Q9QVDO ck:	<x{c x{ 1; MA</x{c 	Q99KX5 ck:	1:	Q923H1 ck:	- X{0 - x{ 1: MA	Q61159 ck:	-x{0 -x{ 1: LE	Q63985 ck:	1: x{C	Q62256 ck:
8137 len: 35 ! Q6653	ck: 4484 len: 19 ! Q65747 <x{0,20}(a,d,e,f,g,i,n,s,v)(0,< td=""><td>(A,D,E,F,G,I,N,)DRx{15} LDDRSKMPYTDAVIH</td><td>4925 len: 25 ! Q61461</td><td><pre><x{0,20}(a,d,e,f,g,i,n,s,v){0, (d)(w)(e)drx{12}="" dwedrnfiaagpltndl<="" pre=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,></pre></td><td>1363 len: 17 ! Q9qv71</td><td><pre><x(0,20)(a,d,e,f,g,i,n,s,v)(0,1)(a,d, eisfqlgvefdevtaddrkvksvvtldggklv<="" pre="" x(14)(d)drx(14)=""></x(0,20)(a,d,e,f,g,i,n,s,v)(0,1)(a,d,></pre></td><td>581 len: 32 ! Q9qv89</td><td><pre><x{0,20}(a,d,e,f,g,i,n,s,v){0 pre="" xxesxkgrxtegfnadrkxqxxel<="" x{14}(a)drx{7}=""></x{0,20}(a,d,e,f,g,i,n,s,v){0></pre></td><td>3385 len: 24 ! Q9qvd0</td><td><pre><x{0,20}(a,d,e,f,g,i,n,s,v)(0, maslpvvgsqvpadrgylgprpavqeh<="" pre="" x(12)(a)drx{12}=""></x{0,20}(a,d,e,f,g,i,n,s,v)(0,></pre></td><td>9106 len: 27 ! Q99kx5</td><td><pre><x(0,20)(a,d,e,f,g,i,n,s,v)(0,1)(a,d,e,h,i pre="" ptpavegavasgaladpataaadrrassiaaxgsrprsmp<="" x(19)(a)drx(16)=""></x(0,20)(a,d,e,f,g,i,n,s,v)(0,1)(a,d,e,h,i></pre></td><td>2032 len: 40 ! Q923h1</td><td><pre><x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a maasmcdvfsfcvgvadrargsvevryvdsik<="" pre="" x{15}(a)drx{14}=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a></pre></td><td>837 len: 32 ! Q61159</td><td><pre><x{0,20}(a,d,e,f,g,i,n,s,v){0, pre="" tfnmyltrerrleisrsvhltdrqv<="" x{20}(t)dbx{2}=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,></pre></td><td>5721 len: 25 ! Q63985</td><td><pre><x{0,20}(a,d,e,f,g,i,n,s,v){0, mssgkqdspwedrippgr<="" pre="" x{10}(e)drx{5}=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,></pre></td><td>3193 len: 18 ! Q62256</td></x{0,20}(a,d,e,f,g,i,n,s,v)(0,<>	(A,D,E,F,G,I,N,)DRx{15} LDDRSKMPYTDAVIH	4925 len: 25 ! Q61461	<pre><x{0,20}(a,d,e,f,g,i,n,s,v){0, (d)(w)(e)drx{12}="" dwedrnfiaagpltndl<="" pre=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,></pre>	1363 len: 17 ! Q9qv71	<pre><x(0,20)(a,d,e,f,g,i,n,s,v)(0,1)(a,d, eisfqlgvefdevtaddrkvksvvtldggklv<="" pre="" x(14)(d)drx(14)=""></x(0,20)(a,d,e,f,g,i,n,s,v)(0,1)(a,d,></pre>	581 len: 32 ! Q9qv89	<pre><x{0,20}(a,d,e,f,g,i,n,s,v){0 pre="" xxesxkgrxtegfnadrkxqxxel<="" x{14}(a)drx{7}=""></x{0,20}(a,d,e,f,g,i,n,s,v){0></pre>	3385 len: 24 ! Q9qvd0	<pre><x{0,20}(a,d,e,f,g,i,n,s,v)(0, maslpvvgsqvpadrgylgprpavqeh<="" pre="" x(12)(a)drx{12}=""></x{0,20}(a,d,e,f,g,i,n,s,v)(0,></pre>	9106 len: 27 ! Q99kx5	<pre><x(0,20)(a,d,e,f,g,i,n,s,v)(0,1)(a,d,e,h,i pre="" ptpavegavasgaladpataaadrrassiaaxgsrprsmp<="" x(19)(a)drx(16)=""></x(0,20)(a,d,e,f,g,i,n,s,v)(0,1)(a,d,e,h,i></pre>	2032 len: 40 ! Q923h1	<pre><x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a maasmcdvfsfcvgvadrargsvevryvdsik<="" pre="" x{15}(a)drx{14}=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a></pre>	837 len: 32 ! Q61159	<pre><x{0,20}(a,d,e,f,g,i,n,s,v){0, pre="" tfnmyltrerrleisrsvhltdrqv<="" x{20}(t)dbx{2}=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,></pre>	5721 len: 25 ! Q63985	<pre><x{0,20}(a,d,e,f,g,i,n,s,v){0, mssgkqdspwedrippgr<="" pre="" x{10}(e)drx{5}=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,></pre>	3193 len: 18 ! Q62256
8 ebola virus. 3' proximal protein (fr	<pre>/ bluetongue virus. outer coat proteir // bluetongue virus. outer coat proteir //</pre>	),1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,H,N	l mus musculus (mouse). cytochrome p-4	),1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,H,N	l rattus sp. lactase-phlorizin hydrola	),1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,H,N )GGKLV	) rattus sp. slp-l4≈fatty acid-binding	),1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,H,N	) cavia (guinea pigs). vitronectin (fr	),1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,H,N	5 mus musculus (mouse). hypothetical 2	),1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,H,N SSIAAXGSRPRSMP	l cricetulus griseus (chinese hamster)	N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,H,N) RGSVEVRYVDSIK	d mus musculus (mouse). nn8-ag (fragme	),1}(A,D,E,H,I,L,M,Q,S)[0,1](D,E,F,H,N	i rattus sp. hox1.8 homeobox homolog p	),1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,H,N	mus musculus (mouse). spermatogenic-

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                                                                                                                                                                                        073591
                                                                                                                                                                                                                                                                                                                                                                           Q07150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9PWC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q83622
     P83009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q07145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q90298 ck: 9642 len: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q84254
     ck: 7125 len: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ck: 3517 len: 9
                                                                                                                                                                                        ck: 8165 len: 14
                                                                                                                                                                                                                                                                                                                                                                           ck: 9407 len: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ck: 9552 len: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ck: 9410 len: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ck: 9066 len: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ck: 9645 len: 39
                                                                            <X[0,20](A,D,E,F,G,I,N,S,V)[0,1](A,D,E,H,I,L,M,Q,S)[0,1](D,E,F,
x[10](T)DRX
RLEISKSINLTDRQ</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                     <X{0,20}{A,D,E,F,G,I,N,S,V){0,1}{A,D,E,H,I,L,M,Q,S){0,1}{D,E,F,
x{20}{T}DRx{4}
LFNMYLTRERRLEISRGVNLTDRQVKI</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \begin{array}{l} \langle x\{0,20\}\{A,D,E,F,G,I,N,S,V\}\{0,1\}\{A,D,E,H,I,L,M,Q,S\}\{0,1\}\{D,E,F,x\{19\}\{D\}DRx\{17\}\\ LYELLSVLPSQLQPHVESPDDRSFLHAMFGERSLHSLVK \end{array} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <X[0,20](A,D,E,F,G,I,N,S,V)[0,1](A,D,E,H,I,L,M,Q,S)[0,1](D,E,E,
x[4](E)DRX[2]
THYSEDRYL</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \begin{array}{l} <\mathbf{x}\{0,20\}(\mathtt{A},\mathtt{D},\mathtt{E},\mathtt{F},\mathtt{G},\mathtt{I},\mathtt{N},\mathtt{S},\mathtt{V})\{0,1\}(\mathtt{A},\mathtt{D},\mathtt{E},\mathtt{H},\mathtt{I},\mathtt{L},\mathtt{M},\mathtt{Q},\mathtt{S})\{0,1\}(\mathtt{D},\mathtt{E},\mathtt{F},\mathtt{x}\{12\}\{\mathtt{D}\}\mathtt{DRx}\{20\}\\ &\mathtt{MRKINNFLSLKEDDRNLKLKLLICNHTVDSEPHTS} \end{array} 
                                                                                                                                                                                                                                                                                              (x_{0,20},A_D,E,E,G,I,N,S,V)_{0,1},A_D,E,H,I,L,M,Q,S)_{0,1}_{0,E,E,x_{20}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <X{0,20}(A,D,E,F,G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,
x{20}(T)DRx{4}
LENMYLTRERRLEISRSVHLTDRQVKI</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <x\{0,20\}(A,D,E,F,G,I,N,S,V)\{0,1\}(A,D,E,H,I,L,M,Q,S)\{0,1\}(D,E,E,x\{13\}(A)DRx\{6\}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LFSMYLTRERRLEISHLLSLTDRQVKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                x{20}(T)DRx{4}
LFNMYLTRERRLEISKSINLTDRQVKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAGPKPGTTPEDVADRPPDLPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ! Q90298 carassius auratus (goldfish). hom
                                                                                                                                                                                                                                                                                                                                                                     ! Q07150 petromyzon marinus (sea lamprey).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ! Q07145 petromyzon marinus (sea lamprey).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ! Q90297 carassius auratus (goldfish). hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ! 093438 gallus gallus (chicken). lbx1 pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ! Q84254 bovine papillomavirus. x protein
! P83009 lamna nasus. phospholemman (fxv
                                                                                                                                                                                     ! 073591 gallus gallus (chicken). hox.c10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ! Q9pwc1 brachydanio rerio (zebrafish) (ze
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ! Q83622 murray valley encephalitis virus.
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<X{0,20}(A,D,E,F,G,I,N,S,V)(0,1}(A,D,E,H,I,L,M,Q,x{6}(N)(D)DRx{3}

	<pre><x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x,15){a}drx(15) mpvgssipcsistaladrkvvsrywcfftllvl<="" pre=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x,15){a}drx(15)></pre>	1:
	ck: 3787 len: 33 ! Q9ktz5 vibrio cholerae. hypothetical protei	Q9KTZ5
	<pre><x[0,20](a,d,e,f,g,i,n,s,v)[0,1](a,d,e,h,i,l,m,q,s)[0,1](d,e,f,h,n,x[1])(a)drx[12] mpasslgtgspaadrldatherrrevi<="" pre=""></x[0,20](a,d,e,f,g,i,n,s,v)[0,1](a,d,e,h,i,l,m,q,s)[0,1](d,e,f,h,n,x[1])(a)drx[12]></pre>	1 :
	ck: 8577 len: 27   006283 mycobacterium tuberculosis. hypothet	006283
	<pre><x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x;i3){e}drx[7] mspltplrnpltqedrffqeiia<="" pre=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x;i3){e}drx[7]></pre>	1:
	ck: 575 len: 23   025575 helicobacter pylori (campylobacter p	025575
	<pre><x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x,4)(t)drx{2} pre="" sktetdrfd<=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x,4)(t)drx{2}></pre>	
	ck: 3335 len: 9 ! Q70140 human immunodeficiency virus type 1.	Q70140
	<pre><x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x{5}(e)drx{17} magrsedrdeellktvrlikllyqs<="" pre=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x{5}(e)drx{17}></pre>	1:
	ck: 5339 len: 25 ! Q9du42 human immunodeficiency virus type 1.	Q9DU42
Total length Total sequences CPU time	<pre><x[0,20](a,d,e,f,g,i,n,s,v)(0,1)(a,d,e,h,i,l,m,q,s)(0,1)(d,e,f,h,n,m,2)(g)(e))bx(18) dggedrdaaveeavlgtggcrtpk<="" pre="" x[2)(g)(e))bx(18)=""></x[0,20](a,d,e,f,g,i,n,s,v)(0,1)(a,d,e,h,i,l,m,q,s)(0,1)(d,e,f,h,n,m,2)(g)(e))bx(18)></pre>	1:
SPIREMBL.	ck: 2489 len: 24 ! Q9prv3 gallus gallus (chicken). nap-185 neu	Q9PRV3
Databases search	<x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,y 16){e}drx{4} x{16}(E)DRX{4} LASDLLEWIRRTIPWLEDRSPQK</x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,y 16){e}drx{4} 	1:
<u>,</u> ,	ck: 1521 len: 23   Q9ps32 gallus gallus (chicken). nonmuscle a	Q9PS32
091	<pre><x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x{4}(t)drx{13} ieyytdreiqsnvgskvhly<="" pre=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x{4}(t)drx{13}></pre>	1:
1.	ck: 6634 len: 20      (09ps38 rana catesbelana (bull frog). po gly	Q9PS38
Q81	<pre><x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x 20){t)drx 4} ffnvyinkekrlqlsrmlnltdrqvki<="" pre=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x 20){t)drx 4}></pre>	<b></b>
<u>, , , , , , , , , , , , , , , , , , , </u>	ck: 9516 len: 27 ! 090zg3 oryzias latipes (medaka fish). hoxc1	Q90ZG3
283	<pre><x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x{7}(e)drx{3}) agepannedreny<="" pre=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x{7}(e)drx{3})></pre>	1:
<b>.</b>	ck: 6920 len: 13   P83010 triakis scyllium (leopard shark) (tr	P83010
Q91	VSDVPNNDDRFTY	1:

Databases searched:
SWISS-PROT, Release 40.3, Released on 9Aug2002, Formatted on 20Aug2002
SPTREMBL, Release 21.0, Released on 15Jun2002, Formatted on 28Jun2002
Total finds:
Total length:
Total length:
247,523,443
Total sequences:
784,472
CPU time:
04:50.37

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! FINDPATTERNS on pir: * allowing 0 mismatches
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x[7](D)DRx[15]
SHRLPTLDDRSKMPYTDAVIHEIQR</pre>
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                                                                                                                                                                                                 ck: 6107 len: 20
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                                                                       ck: 6068 len: 20
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x[6](E)DRx[11]
GKITFYEDRGFQGHCYECSS</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <X{0,20}(A,D,E,F,G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,H,
x{9}(E)Drx{10}
ADEESCCSYEDRREVRHIWDDV</pre>
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x[6](E)DRx[11]
GKITFYEDRGFQGRHYECSS</pre>
                                                                                                                          <X{0,20}(A,D,E,F,G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,H,X{6}(E)DRx{11}
GKIVFYEDRNFQGRSYECSS</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <X[0,20](A,D,E,F,G,I,N,S,V)[0,1](A,D,E,H,I,L,M,Q,S)[0,1](D,E,F,H,
x[7](E)DRx[14]
SSNSCTTEDRREMQLMWANVWSAQ</pre>
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VTVSADVTTTKELLDLADRVMGFVSTRS
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                                                                                                                                                                                                ! gamma-crystallin (total) - siamang
                                                                                                                                                                                                                                                                                                                          ! gamma-crystallin II - milk shark (fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ! gamma crystallin V - bullfrog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ! orotidine-5',-monophosphate decarboxylase -
                                                                     ! gamma-crystallin (total) - Formosa sika de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ! hemoglobin AII - tube worm (Lamellibrachia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ! hemoglobin chain IV - earthworm (Lumbricus
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                                                                                    S35554
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x(16)(T)DRx(10)
EPVVYEQFQFLDGDGWTDRWIESKHKSDF</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \begin{array}{l} & < x\{0,20\}(A,D,E,F,G,I,N,S,V)\{0,1\}(A,D,E,H,I,L,M,Q,S)\{0,1\}\{D,E,F,x\{16\}(T)DRx\{10\}\\ & = PVVYFKEQFLDGDGWTDRWIESKHKSDF \end{array} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <X(0,20)(A,D,E,F,G,I,N,S,V)(0,1)(A,D,E,H,I,L,M,Q,S)(0,1)(D,E,F,
x(15)(D)DRx(18)
GSQDFASQLSKLRLSDDRTADTNRIKRIINMRVLNS</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <X{0,20}(A,D,E,F,G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,
x{16}(T)DRx{5}
EPAIYEKEQFLDGDGXTDRXIESK</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \begin{array}{l} & < x\{0,20\}(A,D,E,F,\mathcal{G},I,N,S,V)\{0,1\}(A,D,E,H,I,L,M,Q,S)\{0,1\}(D,E,F,X\{11\}(E)DRX\{11\} \\ & = EDGFDFPEYDGEDRVIFISLKNYKA \end{array} 
                                                                                                                                         \begin{array}{l} & < \times \{0,20\} (A,D,E,F,G,I,N,S,V) \{0,1\} (A,D,E,H,I,L,M,Q,S) \{0,1\} (D,E,F,X \{9\} (D) DRX \{20\} \\ & \times \{9\} (D) DRX \{20\} \end{array}  ERDQKLSELDDRADALQAGASQFETSAAKLKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <X{0,20}(A,D,E,F,G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,
                                                                                                                                                                                                                                                                              x{9}(D)DRx{20}
ERDQKLSELDDRADALQAGASVFESSAAKLKR
                                                                                                                                                                                                                                                                                                                                                                                                                x{9}(D)DRx{20}
ERDQKLSELDDRADALQAGASQFESSAAKLKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   x{13}(D)DRx{6}
YKKHPAKRTHIENDDRINQIDR
        x(9)(D)DRx(20)
ERDQKLSELDDRADALQAGASQFETSAAKLKR
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                                                                                                                                                                                                                                                                                                                                                        len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             len:
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                                                                                                                                                                                                                      32
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2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ! myonexin - northern leopard frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ! virulence-associated protein (virA 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ! calcium-binding protein - dog (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ! calreticulin, slow twitch skeletal muscl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ! calreticulin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ! DNA-invertase - phage D108
                                                                                ! vesicle-associated membrane protein 2 -
                                                                                                                                                                                                                    ! vesicle-associated membrane protein 2 -
                                                                                                                                                                                                                                                                                                                                                      ! vesicle-associated membrane protein 1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ! vesicle-associated membrane protein 1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uterine - rabbit (fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   re
```

E44621

ck: 9552

len:

27

homeotic protein Hox 10 (clone 10w) -

1: LENWYLTRERRLEISRGVN  F44621 ck: 9407 len: 27 <pre> <a href="mailto:xi=20"><a href="mailto:xi=20"></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></a></pre>
--

<u>..</u> MTTTDRAGLGRQLQMIRGLH

Η. S66213 <X{0,20}(A,D,E,F,G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,X{9}(E)DRx{5}
MKAIAVKRGEDRPVVIE</pre> ck: 1672 len: 17 ! glucose 1-dehydrogenase (EC 1.1.1.47) -

1: S23180 ck: 7956 len: 31 ! carboxypeptidase - Sulfolobus solfataric

:: S29326 ck: 9119 len: 22 <X{0,20}(A,D,E,F,G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,x(5){T)DRX{14} MEYLTTDRSIECGIYLKKIESI ! hypothetical protein 22, psbA 5'-region

1. T10123 ck: 1444 len: 23 <X[0,20](A,D,E,F,G,I,N,S,V)[0,1](A,D,E,H,I,L,M,Q,S)[0,1](D,E,F,
x[4](A)Drx[16]
NGSQADRSVGQKLAPHLNVRPSI</pre> ! probable catalase (EC 1.11.1.6) - cucumb

<u>..</u> PS0212 ck: 8963 len: 15 <X{0,20}(A,D,E,F,G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,x{2}(D)DRx{9}
SPADDRRDVGDRYAD</pre> ! 29K protein 4228 - rice (strain Nihonbar

Н

Н

-в60698 ck: 2526 len: 29 <X{0,20}(A,D,E,F,G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,
x{13}(E)DRx{13}
DPLDRLLSTLTDLEDRYVAEQKEDDAKNQ</pre> ! trichocyst protein 27 - Paramecium tetra

٠. S19614 ck: 1820 len: 17 <X{0,20}(A,D,E,F,G,I,N,S,V)(0,1}(A,D,E,H,I,L,M,Q,S)(0,1)(D,E,F,
x{7}(E)DRx{7}
GMKXXSMEDRKTVLADW</pre> ! globin - polychaete (Eudistylia vancouve

A60741 ck: 4352 len: 25 ! insulin-like growth factor-binding prote

<u>..</u> B28457 ck: 4360 len: 19 <X{0,20}(A,D,E,F,G,I,N,S,V){0,1}(A,D,E,H,I,L,M,Q,S){0,1}(D,E,F,X{11}(D)DRX{5}
DEAXGIAPEVPDDRPFEPS</pre> <X[0,20](A,D,E,F,G,I,N,S,V)[0,1](A,D,E,H,I,L,M,Q,S)[0,1](D,E,F,
x[20](E)DRx[2]
LAPGPGQGVQAGXPGGXVEEEDRGG</pre> ! proteoglycan II, bone - human (tentative

 $\vdash$ 

1:

1. C54037 ck: 1565 len: 29  $\begin{array}{l} <\mathbf{x}\{0,20\}(\mathtt{A},\mathtt{D},\mathtt{E},\mathtt{F},\mathtt{G},\mathtt{I},\mathtt{N},\mathtt{S},\mathtt{V})\{0,1\}(\mathtt{A},\mathtt{D},\mathtt{E},\mathtt{H},\mathtt{I},\mathtt{L},\mathtt{M},\mathtt{Q},\mathtt{S})\{0,1\}(\mathtt{D},\mathtt{E},\mathtt{F},\mathtt{x}\{17\}(\mathtt{E})\mathtt{DRx}\{9\}\\ & \mathtt{PQLTQEELEAKQAKQKLEDRLAAAAREKL} \end{array}$ ! splicing regulatory protein SWAP homolog

• 'n

<pre>ck: 2627 len: 8</pre>	PT0547
<x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n x{6}(A)DRx CAVAGGADRL</x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n 	1:
ck: 3993 len: 10 ! T-cell receptor alpha chain V-J region (4-1	PT0212
<pre><x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x,4)(a)dbx{13} ntegadrltegkgtqliiqp<="" pre=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x,4)(a)dbx{13}></pre>	1:
ck: 6013 len: 20 ! T-cell receptor alpha chain J region (80)	S03505
<pre><x{0,20}{a,d,e,f,g,i,n,s,v}{0,1}{a,d,e,h,i,l,m,q,s}{0,1}{d,e,f,h,n x{8}{A,DRx{4}} CALSDQGGADRLTFG</x{0,20}{a,d,e,f,g,i,n,s,v}{0,1}{a,d,e,h,i,l,m,q,s}{0,1}{d,e,f,h,n </pre>	1:
ck: 8864 len: 15 ! T-cell receptor alpha chain (PE5.1.1V-alpha	РН0806
<pre><x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x 10){a}drx{4} cavsmneyrgadrltfg<="" pre=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x 10){a}drx{4}></pre>	<b>:</b>
ck: 1531 len: 17 ! T-cell receptor alpha chain (K1 V-alpha-3.p	РН0794
<pre><x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x{8}(a))gx{4} calsetggadrlffg<="" pre=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x{8}(a))gx{4}></pre>	::
ck: 8887 len: 15 ! T-cell receptor alpha chain (C11) - mouse (	РН0780
<x[0,20](a,d,e,f,g,i,n,s,v)[0,1](a,d,e,h,i,l,m,q,s)[0,1](d,e,f,h,n,x 10](b)drx[5] td="" wsskqdspwedrippgr<=""><td>1:</td></x[0,20](a,d,e,f,g,i,n,s,v)[0,1](a,d,e,h,i,l,m,q,s)[0,1](d,e,f,h,n,x 10](b)drx[5]>	1:
ck: 3193 len: 18 ! hypothetical protein (proenkephalin 5' regi	A35678
<x(0,20)(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x(18){e)drx(17) MTPSFSGSSKQLQRNAQMEDRGPNHPSEFITGDNLLKT</x(0,20)(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x(18){e)drx(17) 	1:
ck: 6375 len: 38 ! hypothetical protein gadd7.1 - long-tailed	S68260
<pre><x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x,g){e,drx{6}} miglgtdedrlieiil<="" pre="" x{6}(e)drx{6}=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x,g){e,drx{6}}></pre>	<b>:</b> :
ck: 7 len: 16 ! annexin 36K chain - pig (fragment)	A26393
<pre><x[0,20](a,d,e,f,g,i,n,s,v)[0,1](a,d,e,h,i,l,m,q,s)[0,1](d,e,f,h,n,x(14)(a)drx(8) aqesxkgrvtegfnadrkqqqdelx<="" pre=""></x[0,20](a,d,e,f,g,i,n,s,v)[0,1](a,d,e,h,i,l,m,q,s)[0,1](d,e,f,h,n,x(14)(a)drx(8)></pre>	1:
ck: 4810 len: 25 ! vitronectin - dog (fragment)	S22228
<pre><x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x{13}(a)drx{7}) pre="" rgrangtdapragadctf<=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,h,n,x{13}(a)drx{7})></pre>	1:
ck: 9975 len: 23 ! sterol regulatory element 1 binding protein	A48845

1: PT0676	<pre>x(S)(S)(A)DRx ASSDADRG ck: 2049 len: 7</pre>
1:	<pre><x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,x{2}(g)(e)drx asgedrg<="" pre=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,x{2}(g)(e)drx></pre>
PT0576	ck: 2172 len: 7 ! T-cell receptor beta chain V-D-J region
1:	<pre><x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,x(s)(s)(d)drx assddrt<="" pre=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,x(s)(s)(d)drx></pre>
PT0366	ck: 480 len: 28 ! T-cell receptor beta chain V-J region (6
1:	<pre><x[0,20](a,d,e,f,g,i,n,s,v)(0,1)(a,d,e,h,i,l,m,q,s)(0,1)(d,e,f, td="" x{7}(e)drx(18)<=""></x[0,20](a,d,e,f,g,i,n,s,v)(0,1)(a,d,e,h,i,l,m,q,s)(0,1)(d,e,f,></pre>
A46592	ck: 1363 len: 17 ! lactase-phlorizin hydrolase, 200K isofor
<del>!</del>	<pre><x{0,20}{a,d,e,f,g,i,n,s,v){0,1}{a,d,e,h,i,l,m,q,s){0,1}{d,e,f, (D){W}(E)Rx{12} DWEDRNFIAAGPLINDL</x{0,20}{a,d,e,f,g,i,n,s,v){0,1}{a,d,e,h,i,l,m,q,s){0,1}{d,e,f, </pre>
S78414	ck: 6086 len: 26   ribosomal protein RL25, mitochondrial [v
1:	<pre><x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,x{19}(e)drx{4}) isrrxekknkivypdqldgedrrdae<="" pre=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,x{19}(e)drx{4})></pre>
S22227	ck: 5585 len: 25 ! vitronectin - guinea pig (fragment)
<b>1</b> ::	<pre><x[0,20](a,d,e,f,g,i,n,s,v)[0,1](a,d,e,h,i,l,m,q,s)[0,1](d,e,f, pre="" x[14](a)drx[8]="" xxesxkgrxtegfnadrkxqxxelx<=""></x[0,20](a,d,e,f,g,i,n,s,v)[0,1](a,d,e,h,i,l,m,q,s)[0,1](d,e,f,></pre>
A54226	ck: 6170 len: 26 ! light-harvesting protein B-830 alpha-1 c
<u>.</u> 	<pre><x{0,20}{a,d,e,f,g,i,n,s,v}{0,1}{a,d,e,h,i,l,m,q,s}{0,1}{d,e,f, mkvpvmmadenaklnnpeddrkkffv<="" pre="" x{18}{d}drx{5}=""></x{0,20}{a,d,e,f,g,i,n,s,v}{0,1}{a,d,e,h,i,l,m,q,s}{0,1}{d,e,f,></pre>
в54226	ck: 634 len: 23 ! light-harvesting protein B-830 alpha-2 c
1:	<pre><x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,x{18}(d)drx{2})< td=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f,x{18}(d)drx{2})<></pre>
T46593	ck: 6757 len: 38 ! phytoene dehydrogenase [imported] - Myco
1:	<pre><x(0,20)(a,d,e,f,g,i,n,s,v)(0,1)(a,d,e,h,i,l,m,q,s)(0,1)(d,e,f pre="" vpgvgvpttlisgrlaadritgnttrsirhldlkaqls<="" x(15)(a)drx(19)=""></x(0,20)(a,d,e,f,g,i,n,s,v)(0,1)(a,d,e,h,i,l,m,q,s)(0,1)(d,e,f></pre>
н85575	ck: 6940 len: 13 ! hypothetical protein Z0899 [imported] -
1:	<pre><x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f mstdrkpvmllfh<="" pre="" x(s)(t)drx{8}=""></x{0,20}(a,d,e,f,g,i,n,s,v){0,1}(a,d,e,h,i,l,m,q,s){0,1}(d,e,f></pre>

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R;Dick, L.R.; Moomaw, C.R.; Pramanik, B.C.; DeMartino, G.N.; Slaughter, C.A. Biochemistry 31, 7347-7355, 1992
A;Title: Identification and localization of a cysteinyl residue critical for the trypsin-like catalytic activity of the proteasome.
A;Reference number: A42762; MUID:92378961; PMID:1510924
A;Accession: F42762
                                                                                                                                                                                                Curr. Genet. 27, 536-540, 1995
A;Title: A novel strategy for the isolation of defined proceeding of the development of a site-specific integration system for a fireference number: S55729; MUID:96031709; PMID:7553938 A;Accession: S55729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:K02409; NID:g192896; PIDN:AAA37510.1; PID:g553905 A;Note: the authors translated the codon CTA for residue 5 as Pro, ACC for residue 7 as Ser and AGT for residue 12 as Thr C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology C;Keywords: electron transfer; heme; monooxygenase; oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Aspergillus awamori
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change
C;Accession: S55729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein A; Residues: 1-20 <DIC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Bos primigenius taurus (cattle)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 03-Jun-2002
C;Accession: F42762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       !!AA_SEQUENCE 1.0
E1;F42762 - C 3.4.25.1 proteasome endopeptidase complex () subunit 13 - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-25 <STU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytochrome p-450b.
A;Reference number: A21630; MUID:84207435;
A;Accession: A21630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Characterization of a cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Stupans, I.; Ikeda, T.; Kessler, D.J.; Nebert, D.W. DNA 3, 129-137, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F1;A21630 - cytochrome P450b - mouse (fragment)
N;Contains: oxidoreductase (EC 1.-.-.)
C;Species: Mus musculus (house mouse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 11-Jun-1999
                                                                                                               A; Molecule type: DNA
A; Residues: 1-18;19-28 <GOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F1:S55729 - orot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                         R;Gouka, R.J.; Hessing, J.G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     !!AA_SEQUENCE 1.0
                                                                                                                                                                                                                                                                                                                                                 C.A.M.J.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F42762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A21630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transmembrane protein
                                                         decarboxylase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (fragments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: sequence extracted from NCBI backbone (NCBIP:112175); Superfamily: multicatalytic endopeptidase complex chain C9
                                                                                    Superfamily: orotidine-5'-phosphate decarboxylase; orotidine-5'-phosphate
                                                                                                                                                                        Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: A21630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 25 December 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 20
Length:
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   December 22,
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   2002 19:21
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Aspergillus awamori.
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Pl;844336 - neuro

neurotoxin Tx3-2 -

spider (Phoneutria nigriventer)

A; Accession: D60894

VTVSADVTTT KELLDLADRV MGFVSTRS

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C;Species: Phoneutria nigriventer
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Aug-1998
C;Accession: B44336
R;Cordeiro M do, N.; de Figueiredo, S.G.; Valentim A do, C.; Diniz, C.R.; vc.
Eickstedt, V.R.; Gilroy, J.; Richardson, M.
Toxicon 31, 35-42, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Suzuki, T.; Takagi, T.; Ohta, S.
Biochem. J. 255, 541-545, 1988
A;Title: N-terminal amino acid sequence of the deep-sea remarkably resembles that of annelid haemoglobin.
A;Reference number: S01807; MUID:89076216; PMID:3202832
A;Accession: S01808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. J. 241, 441-445, 1987
A;Title: Two globin strains in the giant annelid extracellular haemoglobins.
A;Reference number: A90337; MUID:87241210; PMID:3593201
A;Accession: B28563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F1;S01808 - hemoglobin AII - tube worm C;Species: Lamellibrachia sp. C;Date: 31-Dec-1991 #sequence_revision
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A;Accession: B44336
A;Title: The protein sequence homology of gamma-crystallins among vertebrate classes and their DNA sequence homology to heat-shock A;Reference number: A60894; MUID:89351593; PMID:3255376
                                                                                                                                                       C; Species: Rana catesbeiana (bullfrog)
C; Date: 31-Dec-1993 #sequence_revision
                                                                                                                                                                                                           !!AA_SEQUENCE 1.0
F1:D60894 - gamma
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A;Residues: 1-24 <SUZ>
C;Superfamily: globin; globin homology
C;Keywords: oxygen carrier
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A; Residues: 1-22 <GOT>
C; Superfamily: globin; globin
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                                                                               R;Chiou, S.H.
J. Protein Chem. 7, 527-534, 1988
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A; Reference number: A61570; MUID:89152306; PMID:: A; Recession: A61570
A; Molecule type: protein
A; Residues: 1-20 <CHI>
A; Note: 8-Glu, 9-Gln, 10-Ala, 15-Ser, 18-Thr, and A; Note: this preparation appears to represent the crystallin genes from one specimen C; Superfamily: beta-crystallin C; Keywords: duplication; eye lens
                                      A;Molecule type: protein
A;Residues: 1-20 <CHI>
A;Note: 6-Phe, 14-His, and 15-Cys were also:
A;Note: this preparation appears to represencystallin genes from one specimen
C;Superfamily: beta-crystallin
C;Keywords: duplication; eye lens
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F1:B61570 - gamma-crystallin (total) - Formosa sika deer (fragment)
C:Species: Cervus nippon taiouanus (Formosa sika deer)
C:Date: 25-Oct-1994 #sequence_revision 06-Jan-1995 #text_change 21-Nov-1997
C:Accession: B61570
                                                                                                                                                                                            A;Reference number: A61570; MUID:89152306; PMID:3229121 A;Accession: B61570
                                                                                                                                                                                                                                                         A; Title: Biochemical characterization of
                                                                                                                                                                                                                                                                            R;Chiou, S.H.; Chang, W.P.; Ting, L.M.; Lai, T.A.; Lin, H.K. Curr. Eye Res. 7, 1017-1022, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Residues: 1-20 <CHI>
C:Superfamily: beta-crystallin
C;Keywords: duplication
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A;Title: Characterization of gamma-crystallins from eye lenses of shark: closer structural similarity to mammalian than other piscine gamma-crystallins?
A;Reference number: S04621; MUID:89290026; PMID:2737298
A;Recession: S04621
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C:Species: Rhizoprionodon acutus (milk shark)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 21-Nov-1997
C:Accession: S04621
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A; Residues: 1-20 <CHI>
C; Superfamily; beta-crystallin
C; Keywords: duplication; eye lens
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F1;S04621 - gamma
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## GKITFYEDRG FQGRHYECSS

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J. Biol. Chem. 266, 7155-7165, 1991
A;Title: Calreticulin, and not calsequestrin, is the major calcium binding protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic ret. A;Reference number: A33208; MUID:91201375; PMID:2016321
A;Accession: E33208
                                                A; Note: hepatic form C; Superfamily: calreticulin
                                                                                             A; Molecule type: protein A; Residues: 1-20 <MI2>
                                                                                                                                                                                                         A; Molecule type:
A; Residues: 1-29
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J.E.; Opas, M.; Michalak, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  !!AA_SEQUENCE 1.0

F1;E33208 - calreticulin, uterine - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Jul-1991 **sequence_revision 31-Jul-1991 **t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Comment: This protein resembles calsequestrin in sequence but distribution and physical properties.
C;Superfamily: calsequestrin
C;Keywords: fibronectin binding; glycoprotein; skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dev. Biol. 142, 103-114, 1990
A; Title: Myonexin: an 80-kDa glycoprotein at embryonic myotendinous junctions.
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C;Species: Rana pipiens (northern leopard frog)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Jul-1999
C;Accession: A60502; A33087
                                                                                                                                        A; Status: preliminary
                                                                                                                                                                 A; Note: uterine form A; Accession: F33208
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       E33208
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J. Biol. Chem. 266, 7155-7165, 1991
A:Title: Calreticulin, and not calsequestrin, is the major protein of smooth muscle sarcoplasmic reticulum and liver A;Reference number: A33208; MUID:91201375; PMID:2016321
A;Accession: C33208
                                                                                                                                                                                                                                                                                                                           F1;C33208 - calreticulin, slow twitch skeletal muscle - C:Species: Oryctolagus cuniculus (domestic rabbit) C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text C:Accession: C33208
                                                 C; Superfami
C; Keywords:
                                                                                           A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-29 <MIL>
                                                                                                                                                                                                                                                                                 R;Milner, R.E.; Baksh, S.; Shemanko, C.; Carpenter, M.R.; J.E.; Opas, M.; Michalak, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                   !!AA_SEQUENCE 1.0
    C33208
                                              Superfamily: calreticulin Keywords: skeletal muscle
  Length: 29
  December 22,
  2002 19:21
Type:
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endoplasmic reticulum
2871
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Type:

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8909

EPVVYFQFQF

LDGDGWTDRW IESKHKSDF

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A;Gene: gin
C;Superfamil
C;Keywords:
      C; Specie
C; Date:
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C;Date:
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Nucleic Acids Res. 15, 6691-6704, 1987
A;Title: The right end of transposable bacteriophage D108 contains pair protein-encoding sequence not present in bacteriophage Mu. A;Reference number: S07394; MUID:87316928; PMID:2957646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F1;A33434 - calcium-binding protein - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 21-Feb-1990 #sequence_revision 21-Feb-1990 #text_C;Accession: A33434
R;Collins, J.H.; Xi, Z.; Alderson-Lang, B.H.; Treves, S.;
Biochem. Biophys. Res. Commun. 164, 575-579, 1989
                                            F1:S35552 - vesic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: phage D108
A;Note: host Escherichia coli
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change
C;Accession: S07394
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A; Residues: 1-36 <GUL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Gulig, P.A.; Chiodo, V.A.
Infect. Immun. 58, 2651-2658,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         !!AA_SEQUENCE 1.0
F1;B41481 - virulence-associated protein
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C;Keywords: calcium binding
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A;Title: Sequence homology of a cantigen
calregulin and the human Ro/SS-A antigen
A;Reference number: A33434; MUID:90026437; PMID:2803321
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A; Residues: 1-22 <SZA>
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F1;S07394 - DNA-1
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                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X05926; NID:g14918;
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    1;S35552 - vesicle-associated membrane protein 1 -;Species: Mus musculus (house mouse);Date: 10-Dec-1993 #sequence_revision 27-Feb-1997 #
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27-Feb-1997 #text_change 17-Mar-1999
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                                            mouse (fragment)
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A; Reference number: S35552; MUID:93354436; A; Accession: S35553
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C;Species: Gallus gallus (chicken)
C;Date: 20-May-1994 #sequence_revision
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A; Residues: 1-32 < PAT>
C; Superfamily: synaptobrevin
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                                                         A; Molecule type: DNA
A; Residues: 1-32 < PAT>
                                                                                                            A;Title: Neurotransmission and secretion. A;Reference number: S35552; MUID:93354436; A;Accession: S35554
                                                                                                                                                                        R; Patarnello, T.; Bargelloni, L.; Nature 364, 581-582, 1993
                                                                                                                                                                                                           C; Accession: S35554
                                                                                                                                                                                                                           F1;S35554 - vesicle-associated membrane protein 2 - C;Species: Mus musculus (house mouse)
C;Date: 10-Dec: 1993 #sequence_revision 27-Feb-1997 #
                                                                                                                                                                                                                                                                                                                                                                                                     C; Keywords: membrane
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A; Residues: 1-32 < PAT>
C; Superfamily: synaptobrevin
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Nature 364, 581-582, 1993
A;Title: Neurotransmission and secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: S35555
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C;Date: 10-Dec-1993 #sequence_revision 26-Jul-1996 #text_change 17-War-1999
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A; Residues: 1-32 < PAT>
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Nature 364, 581-582,
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Nature 364, 581-582, 1993
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                                   C; Superfamily: synaptobrevin
                                                                                           A; Status: preliminary
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!!AA\_SEQUENCE 1.0
F1;E44621 - homeotic

protein Hox 10

(clone 10w)

sea

lamprey (fragment)

ERDQKLSELD

DRADALQAGA

SQFETSAAKL KR

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i!AA_SEQUENCE 1.0
P1;E64634 - hypothetical prote
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_
C;Accession: E64634
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A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D. Lasky, S.R.; Baliga, N.; Thorsson, V.; Sbrogna, J.; Swartzell, S.; Weir, D.; Hall, J.; Dahl, T.A.; Welti, R.; Goo, Y.A.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablonski, P.E.; Krebs, M.P.; Angevine, C.M.; Dale, H.; Isenbarger, T.A.; Peck, R.F.; Pohlschrod, M.; Spudich, J.L.; Jung, K.H.; Alam, M.; Freitas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 1216-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe. T.M.; Liang, P.; Riley, M.; Hood, L.; DasSarma, S.
A:Title: Genome sequence of Halobacterium species NRC-1.
A; Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: C84355
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A;Title: Expansion of the Hox gene family and the evolution of chordates. A;Reference number: A44616; MUID:93317669; PMID:8101001
A;Accession: F44621
A;Accession: F44621
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El;F44651 - homeotic protein Hox 10 (clone 10x) - sea lamprey (fragment)

C:Species: Petromyzon marinus (sea lamprey)

C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 15-Oct-1999

C:Accession: F44621
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C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 15-Oct-1999
C;Accession: E44621
R;Pendleton, J.W.; Nagai, B.K.; Murtha, M.T.; Ruddle, F.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 6300-6304, 1993
A;Title: Expansion of the Hox gene family and the evolution of chordates.
A;Reference number: A44616; MUID:93317669; PMID:8101001
A;Accession: E44621
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A; Residues: 1-32 <STO>
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C;Accession: C84355
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A; Residues: 1-27 < PEN>
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A; Residues: 1-27 <PEN>
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                                  #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
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                                                                                                          protein HP0917 - Helicobacter pylori (strain 26695)
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N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequer
C;Accession: A82288
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A;Title: The genetic organization of the mau gene cluster of autotroph Paracoccus denitrificans.
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F1;PH0858 - MauD protein - Paracoccus denitrificans (fragment)

C;Species: Paracoccus denitrificans

C;Date: 17-Aug-1992 *sequence_revision 17-Aug-1992 *text_change 08-Oct-1999
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Nature 388, 539-547, 1997
A;Autbors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.M.; Venter, J.C.
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A; Accession: A61412
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R;Rosenzweig, A.C.; Lippard, S.J.
Acc. Chem. Res. 27, 229-236, 1994
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                                                                                                                                                         !!AA_SEQUENCE 1.0
                                                                                                                                                                                                                                                                                                                                            C; Keywords: oxidoreductase
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A; Residues: 1-23 <CHI>
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    hypothetical protein VC0735 [imported] -

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#sequence\_revision 20-Aug-2000

#text\_change 02-Feb-2001

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C;Species: Vibrio che
C;Date: 18-Aug-2000 #
C;Accession: B82421
R;Heidelberg, J.F.; F
                                                                                            from Thiocapsa roseopersicina.
A; Reference number: A39089; MUID:91093297; PMID:1845998
A; Accession: B39089
                                                                                                                                                                                            R;Kovacs, K.L.; Tigyi, G.; Thanh, L.T.; Lakatos, S.; Kiss, Z.; Bagyinka, C. J. Biol. Chem. 266, 947-951, 1991
A;Title: Structural rearrangements in active and inactive forms of hydrogenase
                                                                                                                                                                                                                                                                                            C; Species: Thiocapsa
C; Date: 27-Nov-1991
C; Accession: B39089
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Dodson, R.J.; Haft, D.H.; Hickey, Etcrson, J.D.; Umayam, L.A.; Gill,
S.R.; Nelson, K.E.; Read, T.D.; Tettelln, H.; Richardson, D.; Ermolaeva, M.D.;
Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.; McDonald, L.;
Utterback, T.; Fletshmann, R.D.; Nierman, W.C.; White, O.; Salzberg, S.L.;
Smith, H.O.; Colwell, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 405, 477-483, 2000
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A; Molecule type: protein A; Residues: 1-20 < KOV>
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A; Residues: 1-32 <HEI>
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A;Accession: B82421
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GSPDB:GN00126; TIGR:VC0735
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A; Residues: 1-33 <HEI>
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A;Accession: A82288
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                                                            A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    !!AA_SEQUENCE 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Umayam, L.A.; Gill, S.R.; Nelson, K.E.; Read, T.D.; Tettelin, H.; Richardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.; McDonald, L.; Utterback, T.; Fleishmann, R.D.; Nierman, W.C.; White, O.; Salzberg, S.L.; Smith, H.O.; Colvell, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N16961 serogroup 01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene: VC0735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 32
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                                                                                                                                                                                                                                                                                                                                                                    Thiocapsa roseopersicina
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                                                                                                                                                                                                                                                                                                                                #sequence_revision 27-Nov-1991 #text_change 23-Jun-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GB:AE003852;
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A;Cross-references: GB:Z95557; GB:AL123456; NID:g3242276; PIDN:CAB08945.1; PID:e316847; PID:g2113977
                                                                                                                                                                                                                                                                                                      Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the
A; Experimental source: strain H37Rv
                                                                                                                                                                                                   A;Reference number: A70500; MUID:98295987; PMID:9634230 A;Accession: H70954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Cole, S.T.; Brosch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: H70954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Mycobacterium tuberculosis
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                                                                                                   A; Residues: 1-27 <COL>
                                                                                                                                A; Molecule type: DNA
                                                                                                                                                                 A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barry III, C.E.; Tekaia, F.; Badcock, K. Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.;
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Length: 27 December 22, 2002 19:21 Type: Þ Check:

Rv3599c

## MPASSLGTGS PAADRLDATH ERRREVI

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A;Title: An acyl-carrier protein - thioesterase domain from the 6-deoxyerythronolide B synthase of Saccharoplyspora erythraea. production, purification and characterisation in Escherichia co. A;Reference number: S14091; MUID:91153324; PMID:1999200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Saccharopolyspora erythraea C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 21-Nov-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharopolyspora erythraea (fragment)
N;Alternate names: 51K protein
                                                                 A; Description: involved in desosamine biosynthesis C; Keywords: antibiotic biosynthesis; intramolecular oxidoreductase; isomerase
                                                                                                                                                                                                                                        A; Molecule type: protein A; Residues: 1-20 <CAF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: S14161
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                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                             A; Accession: S14161
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                                                                                                                                                                       A;Gene: eryCII
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                                                                                                                                      Function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biochem. 195, 823-830, 1991
Length: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B.; Packman, L.C.; Rawlings, B.J.; Staunton,
19:21 Type: P
   Check:
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R;Bonete, M.J.; Pire, C.; LLorca, F.I.; Camacho, M.L. FEBS Lett. 383, 227-229, 1996 R;Title: Glucose dehydrogenase from the halophilic Archaeon Haloferax mediterranei: enzyme purification, characterisation and N-terminal se

C;Species: Haloferax mediterranei C;Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 30-Oct-1998

- glucose 1-dehydrogenase (EC 1.1.1.47) - Haloferax mediterranei

C; Accession: S66213

!!AA\_SEQUENCE 1.0

MTTTDRAGLG

RQLQMIRGLH

(fragment)

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P1;S23180 -
C;Species: S
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A.;Title: Chloroplast DNA of black pine retains a residual inverted repeat lacking rRNA genes: nucleotide sequences of trnQ, trnK, psbA, trnI and tr the absence of rpsi6.
A;Reference number: S20449; MUID:92212283; PMID:1557027
A;Accession: S29326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:D11467; NID:g344007; PIDN:BAA02023.1; PID:g344011 R;Wakasugi, T.; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiura Proc. Natl. Acad. Sci. U.S.A. 91, 9794-9798, 1994
A;Title: Loss of all ndh genes as determined by sequencing the entire chloroplast genome of the black pine Pinus thunbergii.
A;Reference number: Z16030; MUID:95024047; PMID:7937893
A;Accession: T07427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Purification and characterization of a thermostable carboxypeptidase from the extreme thermophilic archaebacterium Sulfolobus solfataricus.

A;Reference number: S23180; MUID:92283259; PMID:1597179

A;Accession: S23180
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R;Colombo, S.; D'Auria, S.; Fusi, P.; Zecca, L.; Raia,
Eur. J. Biochem. 206, 349-357, 1992
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A; Accession: S66213
A; Status: preliminary
!!AA_SEQUENCE 1.0
F1;T10123 - probable catalase (EC 1.11.1.6) - cucumber (fragment)
C;Species: Cucumis sativus (cucumber)
C;Date: 16-Uul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T10123
R;Toyama, T; Teramoto, H; Takeba, G; Tsuji, H.
Plant Cell Physiol. 36, 1349-1359, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: chloroplast Pinus thunbergiana (Japanese black pine)
C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 18-Aug-2000
C;Accession: S29326; T07427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Tsudzuki, J.; Nakashima, K.; Tsudzuki, T.; Hiratsuka, J.; Wakasugi, T.; Sugirra, M.
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P1;S29326 - hypotl
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A; Residues: 1-31
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                                                                                                                                                                                                                                                                                                                                              A; Genome: chloroplast
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                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-22 <WAK>
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A; Residues: 1-22 <TSU>
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;Species: Sulfolobus solfataricus
;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
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A;Title: Cytokinin induces a rapid decrease in the levels of mRNAs for catalase, 3-hydroxy-3-methylglutaryl CoA reductase, lectin and other unidentified proteins in etiolated cotyledons of cucumber. A;Reference number: 216946; MUID:96104306; PMID:8564304
A;Accession: T10123
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C;Species: Oryza sativa (rice)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
C;Accession: PS0212
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A; Residues: 1-23 <TOY>
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                                     R;Qabar, A.N.; Stern, M.S.; Walz, D.A.; Chiu, J.T.; Timl Kapp, O.H.; Vinogradov, S.N.
J. Mol. Biol. 222, 1109-1129, 1991
A;Title: Hierarchy of globin complexes. The quaternary sextracellular chlorocruorin of Eudistylia vancouverii.
A;Reference number: S19532; MUID:92106333; PMID:1762147
A;Accession: S19614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: B60698
R; Tindall, S.H.; Devito, L.D.;
J. Cell Sci. 92, 441-447, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: germ C; Comment: molecular weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Paramecium tetraurelia C;Date: 28-Apr-1993 #sequence_revision
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F1;B60698 - trichc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: A60698; MUID:90078398; PMID:2592449
A;Accession: B60698
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                                                                                                                                                                                          C; Accession: S19614
                                                                                                                                                                                                                C;Species: Eudistylia vancouveri
C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997
                                                                                                                                                                                                                                                        F1;S19614 - globin - polychaete N;Alternate names: chlorocruorin
                                                                                                                                                                                                                                                                                                                                                                                                                            C; Keywords: extracellular
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A; Molecule type: protein A; Residues: 1-17 < QAB>
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Dryza sativa (rice)
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A; Experi
A; Note:
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F1;B2B457 - proteoglycan II, bone - human (tentative sequence) (
C;Species: Homo sapiens (man)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change
C;Accession: B2B457
                                                                                                                                                                                                    A:Title: Conservation of regulated alternative splicing and identification functional domains in vertebrate homologs to the Drosophila splicing regul suppressor-of-white-apricot.

A:Reference number: A54037; MUID:94266805; PMID:8206918

A:Accession: C54037
                                                                                                                                    A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Residues: 1-29 <DEN>
                                                                                                                                                                                                                                                                                                                             R;Denhez, F.; Lafyatis, R.
J. Biol. Chem. 269, 16170-16179,
                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change
C;Accession: C54037
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E1;C54037 - splicing regulatory
clone pFL2) - human (fragment)
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A; Residues: 1-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Fisher, L.W.; Hawkins, G.R.; Tuross, N.; Termine, J.D. J. Biol. Chem. 262, 9702-9708, 1987
A;Title: purification and partial characterization of sm II, bone sialoproteins I and II, and osteonectin from t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 1-25 <FOR>
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A;Reference number: A60741; MUID:91011238; PMID:1698907
A;Accession: A60741
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J. Endocrinol. 126, 497-506, 1990

A;Title: An insulin-like growth factor-binding protein purified conditioned by a human lung fibroblast cell line (He[39]L) has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 30-Sep-1993
C;Accession: A60741
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C;Keywords: calcium; dodecamer; heme; homotetramer; oxygen carrier
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!!AA\_SEQUENCE 1.0
F1;A48845 - stero!

sterol regulatory

element 1 binding

protein

(alternatively spliced

A; Status: preliminary

A; Molecule type: mRNA

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C; Species: Canis lupus familiaris (dog)
C; Date: 22-Nov-1993 #sequence_revision 29-Aug-1997 #te
C; Accession: S22228
R; Nakashima, N; Miyazaki, K; Ishikawa, M; Yatohgo,
H; Matsumoto, I; Seno, N; Hayashi, M.
Biochim. Biophys. Acta 1120, 1-10, 1992
A; Mittle: Vitronectin diversity in evolution but unifor and size of the core polypeptide.
A; Reference number: C11760.
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A; Title: SREBP-1, a basic-helix-loop-helix-leucine zipper protein transcription of the low density lipoprotein receptor gene.
A; Reference number: A48845; MUID:94006541; PMID:8402897
A; Accession: A48845
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c;Species: Homo sapiens (man)
C;Date: 07-Apr-1994 #sequence_revision
C;Accession: A48845
R;Yokoyama, C.; Wang, X.; Briggs, M.R.;
                                                                  C;Accession: 568260
R;Hollander, M.C.; Alamo, I.; Fornace Jr., A.J.
Nucleic Acids Res. 24, 1589-1593, 1996
A;Title: A novel DNA damage-inducible transcript,
                                                                                                                                                             P1;S68260 - hypothetical protein gadd7.1 - long-tailed hamster C;Species: Cricetulus longicaudatus (long-tailed hamster) C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_chang
A; Reference number: $68260; MUID: 96211359; PMID: 8649973 A; Accession: $68260
                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein A; Residues: 1-16 <GEI>
                                                                                                                                                                                                                                                                                                                                                                                                                             Ca(2)+-dependent membrane-binding proteins.
A; Reference number: A93379; MUID:86203621; PMID:2422556
A; Accession: A26393
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A;Title: A consensus amino-acid sequence repeat in Torpedo and mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Geisow, M.J.; Fritsche, U.; Hexham, J.M.; Dash,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Sus scrofa domestica (domestic pig)
C;Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 18-Jun-1993
C;Accession: A26393
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C;Species: Canis lupus familiaris (dog)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-23 <YOK>
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                                              but lacks a protein product.
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5, 187-197, 1993
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                                                                    growth,
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!!AA_SEQUENCE 1.0

F1;PH0794 - T-cell receptor alpha chain (KI V-alpha-3.pHDS58) - mouse (fragr C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PH0794
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
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A;Title: T cell receptor genes in a series of class I major histocompatibility complex-restricted cytotoxic T lymphocyte clones specific for a Plasmodium berghei nonapeptide: implications for T cell allelic exclusion and antigen-specific repertoire.
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F1,PH0780 - T-cell receptor alpha chain (C11) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Unl-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PH0780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: T cell receptor genes in a series of class I major histocompatibility complex-restricted cytotoxic T lymphocyte clones specific for a Plasmodium berghei nonapeptide: implications for T cell allelic exclusion and
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                                                                                                                                                                                                                                  A;Cross-references: EMBL:X60899
A;Experimental source: T lymphocyte
                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-17 <CAS>
                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: PH0746; A; Accession: PH0794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: T lymphocyte C; Keywords: T-cell receptor
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A; Residues: 1-18 <KIL>
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A; Cross-references: EM
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A; Residues: 1-15 <CAS>
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Mol. Cell. Biol. 10, 3717-3726, 1990
                                                                                             PH0794
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R:Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted in non-obese diabetic mice.
                                                                                                                                                                                                                                                                                                                                                                                  i!AA_SEQUENCE 1.0
P1.PT0212 - T-cell receptor alpha chain V-J region (4-1-E.2) - mouse (fragme F1.PT0212 - T-cell receptor alpha chain V-J region (4-1-E.2) - mouse (fragme C.Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Mus musculus (house mouse)
C;Datc: 17-Jul-1992 #text_change 30-May-1997
C;Accession: PH0806; PH0781
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
                                                                                                                                                                                            A; Reference number: A; Accession: PT0212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: S03505
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Nature 316, 832-836, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F1;S03505 - T-cell receptor alpha chain J region (80) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Decies: Mus musculus (house mouse) C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 30-May-1997 C;Accession: S03505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: PH0746; MUID:92078846; PMID:1836010 A;Accession: PH0806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Casanova, J.L.; Romero, P.; Widmann, C.; J. Exp. Med. 174, 1371-1383, 1991
                                                                                                           C; Keywords: T-cell receptor
                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-10 <NAK>
                                                                                                                                                                                                                                                                                                                                                           C; Accession: PT0212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Keywords: T-cell receptor
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A; Residues: 1-20 <WIN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-15 <CA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL: X60915
A; Experimental source: T lympho
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A; Residues: 1-15 <CA1>
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F1;PH0806 - Ţ-cell receptor alpha chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL: X02859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: PH0781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S03505 Length: 20
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                                              Length: 10
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CAVAGGADRI
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### MUID: 91217621;
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                                                                                                                                                                                                                      PMID:1902501
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                                                 Type:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse (fragment)
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!!AA\_SEQUENCE 1.0
F1;PT0547 - T-cell receptor beta chain V-D-J region (126-1AI) - mouse (fragment)
C;Species: Mus musculus (house mouse)

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A;Reference number: I
A;Accession: PT0676
A;Status: translation
A;Molecule type: DNA
        A:Title: Graft-versus-host resistance induced by class histocompatibility complex-specific T cell clones. A:Reference number: PT0360; MUID:91108330; PMID:1824856 A:Accession: PT0356
A:Molecule type: mRNA
                                                                                                                                                          !!AA_SEQUENCE 1.0
F1;PT0366 - T-cell receptor beta chain V-J region C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 C;Accession: PT0366
R;Lehmann, P.V.; Drexler, K.; Tary-Lehmann, M.; Fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Feeney,
J. Exp. M
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F1;PT0576 - T-cell receptor beta chain V-D-J region
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #
C;Accession: PT0576
                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-7 <FEE>
A; Experimental source:
C; Keywords: T-cell rec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: PT0509; MUII
A;Accession: PT0576
A;Status: translation not shown
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F1;PT0676 - T-cell receptor beta chain V-D-J region (140-1AL) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0676
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A; Residues: 1-7 <FEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: day 18 C; Keywords: T-cell receptor
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J. Exp. M
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A; Residues: 1-8 <FEE>
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A; Title: Junctional sequences of fetal T cell receptor beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regions
                                                                                                                                   Nagy, Z.A.
                                                                                                                                                                                                                                                                                                                                                                                              Experimental source: day 19 Keywords: T-cell receptor
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Exp. Med. 174, 115-124, 1991

The first sequences of fetal T cell receptor beta
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                                                                                                                    Exp. Med. 173, 333-341, 1991
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Exp. Med. 174, 115-124,
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                                                   PMID:1824856
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purpuratum (fragment)
C; Species: Chromatium
C; Date: 05-Jan-1996 #s
C; Accession: A54226
                                                                                                                                                                                                                                                                                              Biochim. Biophys. Acta 1120, 1-10, 1992
A; Title: Vitronectin diversity in evolution but uniform and size of the core polypeptide.
A; Reference number: S21768; MUID:92207982; PMID:1372829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence) (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 25-Feb-1998 #sequence_revision 13-Mar-1998
                                                                                                                                                                                                                                 A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Cavia porcellus (guinea pig)
C;Date: 22-Nov-1993 #sequence_revision
C;Accession: S2227
C;Accession: S2227
R;Nakashima, N.; Miyazaki, K.; Ishikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: the protein is designated as mitochondrial ribosomal protein C;Keywords: mitochondrion; protein biosynthesis; ribosome
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F1;A54226 -!!AA\_SEQUENCE 1.0

light-harvesting protein B-830 alpha-1 chain

Chromatium

#sequence\_revision

05-Jan-1996

#text\_change

05-Jan-1996

A; Accession:

S22227

protein 25

Length:

December

22,

2002

19:

: 21

Type:

Check:

XXESXKGRXT

EGFNADRKXQ XXELX

Matsumoto, I.;

yazaki, K.; Ishikawa, Seno, N.; Hayashi, M. cta 1120, 1-10, 1992

X .

Yatohgo,

Ogawa,

H.; Uchibori,

but uniformity

'n.

ligand binding

29-Aug-1997 #text\_change 29-Aug-1997

!!AA\_SEQUENCE 1.0 F1;S22227 - vitronectin - guinea pig (fragment)

A; Molecule type: protein A; Residues: 1-26 <GOL> A; Accession: S78414 A; Reference number: S78411 R; Goldschmidt-Reisin, S.; submitted to the Protein C; Accession: S78414

s.;

Sequence Graack,

H.R. Database,

February

#text\_change

21-Jul-2000

ribosomal protein RL25, mitochondrial [validated] -

rat

(tentative

S78414

Length: 26

2002

19:21

Type:

שי

Check:

6086

ISRRXEKKNK

IVYPDQLDGE December 22,

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A; Note: sequence extracted from NCBI backbone C; Keywords: carbohydrate digestion; intestine
                                                                                                                                                   A; Molecule type: protein
A; Residues: 1-17 < DUD>
                                                                                                                                                                                                               A; Reference number: A46592; MUID:93293888; PMID:8514793 A; Accession: A46592
                                                                                                                                                                                                                                                                          A; Title:
                                                                                                                                                                                                                                                                                        J. Biol.
                                                                                                                                                                                                                                                                                                         R;Dudley, M.A.; Hachey, D.L.; Quaroni, A.; Hu
Rosenberger, J.; Perkinson, J.S.; Cook, G.;
                                                                                                                                                                                                                                                                                                                                                                F1;A46592 - lactase-phlorizin hydrolase, 200K isoform - rat (fragment) C:Species: Rattus norvegicus (Norway rat) C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 01-Nov-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-28 <LEH>
C;Keywords: T-cell receptor
!!AA_SEQUENCE 1.0
                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                    C; Accession: A46592
                                                                             A46592
                                                                                                                                                                                                                                                 the fed adult rat.
                                                                                                                                                                                                                                                                                          Rosenberger, J.; Perkinson, J.S.; Coordinate Chem. 268, 13609-13616, 1993
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                                                                         Length: 17
                                                                                                                                                                                                                                                                  In vivo sucrase-isomaltase and lactase-phlorizin hydrolase turnover
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Thornber,

J.P.

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!!AA_SEQUENCE 1.0
F1:T46593 - phytoene dehydrogenase [imported] - Mycobacterium marinum (fragment)
C;Spec1es: Mycobacterium marinum
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 21-Jul-2000
C;Accession: T46593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Chromatium purpuratum
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
C;Accession: B54226
R;Kerfeld, C.A.; Yeates, T.O.; Thornber, J.P.
Biochemistry 33, 2178-2184, 1994
A;Title: Purification and characterization of the peripheral antenna of the purple-sulfur bacterium Chromatium purpuratum: evidence of an unusual
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A;Residues: 1-26 <KER>
C;Keywords: antenna complex; light-harvesting
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A;Accession: A54226
A;Status: preliminary
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                                                                                                                                                                                                        !!AA_SEQUENCE 1.0
P1;H85575 - hypothetical pro
O157:H7, substrain EDL933)
C;Species: Escherichia coli
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A; Residues: 1-23 <KER>
C; Keywords: antenna complex; light-harvesting polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pigment-protein composition. A; Reference number: A54226; MA; Accession: B54226
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, G.F.; Evans, P.S.; Gregor, J.; Kirkpatrick, H.A.; Posfai, G.; Hackett, J.; Klink, S.; Boutin, A.; Shao, Y.; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, J.; Anantharar T.S.; Lin, J.; Yen, G.; Schwartz, D.C.; Welch, R.A.; Blattner, F.R.
                                                                                                                                               C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: H85575
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F1;B54226 - light-harvesting protein B-830 alpha-2 chain -
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Biochemistry 33, 2178-2184, 199
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A;Experimental source: strain M
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A;Description: Separation and characterization of Arabidopsis two-dimensional gel electrophoresis.
A;Reference number: PA0001
A;Accession: PA0041
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F1;PA0041 - plastoquinol-plastocyanin reductase (EC
F1;PA0041 - plastoquinol-plastocyanin reductase (EC
thallana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: 30-Jun-1992 #sequence_revision 06-Jan-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Genome sequence of enterohemorrhagic Escherichia A; Reference number: A85480; MUID:21074935; PMID:11206551 A; Accession: H85575
                                                                                                                                                                                                                            R; Kamo, M.; Kawakami, T.; Miyatake, submitted to JIPID, July 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE005174; NID:g12513665; PIDN:AAG55068.1; GSPDB:GN00145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-13 <STO>
                                              C; Keywords: oxidoreductase
                                                                      A; Experimental source: lea:
                                                                                           A; Molecule type: protein A; Residues: 1-15 < KAM>
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PA0041 Length: 15
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AC P81823;
DT 30-MAY-2000 (R
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RAP SEQUENCE.
RC TISSUE-Cerebra
RX MEDLINE-981211
RAP SEQUENCE.
RT TISSUE-Cerebra
RX MEDLINE-981211
RAP DUVE H. Johns
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RT allatostatin s
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RI EUR. J. Bioche
CC -i- FUNCTION:
CC -i- SIMILARITY
KW Neuropeptide:
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SQ SEQUENCE 27
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
AMP deaminase 1 (EC 3.5.4.6) (Myoadenylate
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-i- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
-i- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carcinus Maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
Brachyura; Eubrachyura; Portunoidea; Portunidee; Carcinus.
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-!- FUNCTION: AMP DEAMINASE PLAYS A CRITICAL ROLE IN ENERGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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MOD_RES 27 27 AMIDATION (POTENTIAL)
P81072;
                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PATHWAY: PURINE NUCLEOTIDE CYCLE.
-!- SUBUNIT: HOMOTETRAMER.
-!- SIMILARITY: BELONGS TO THE ADENOSINE AND AMP DEAMINASES FAMILY.
InterPro; IPR001365; A/AMP_deaminase.
PROSITE; PS00485; A_DEAMINASE; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- CATALYTIC ACTIVITY: AMP + H(2)0 = IMP + NH(3).
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                                   AMDI_RABIT
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                                                                                                                                                                                                                                                                                     3195 MW;
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                                                                                                                                                                                                                                                                                     B03E296D63BB6E75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
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                                                                                                                                                                                                           Type: P Check: 7006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Type: P
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA-invertase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
AMP deaminase 1 (EC 3.5.4.6) (Myoadenylate deaminase) (AMP deaminase
                                                                                                                                                                                    Szatmari G.B., Lapointe M., Dubow M.S.;
"The right end of transposable bacteriophage D108 contains a 520 base pair protein-encoding sequence not present in bacteriophage Mu.";
Nucleic Acids Res. 15:6691-6703(1987).
-!- FUNCTION: THIS PROTEIN CATALYZES THE INVERSION OF A 3000-BP
-!- FUNCTION OF PHAGE DNA. THE INVERSION RESULTS IN A MODIFICATION OF THE 3 END OF THE TAIL FIBER GENE AND ALTERS THE HOST SPECIFICITY.
-!- SIMILARITY: BELONGS TO THE SITE-SPECIFIC RECOMBINASE RESOLVASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences of homologous 17-kDa CNBr fragments: autorecognit rabbit anti-{chicken AMPD}.";
Comp. Biochem. Physiol. 116B:371-377(1997).
-i- FUNCTION: AMP DEAMINASE PLAYS A CRITICAL ROLE IN ENERGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97269365; PubMed=9114497; Chilson O.P., Kelly-Chilson A.E., Siegel N.R.; "AMP-deaminases from chicken and rabbit muscle: partial primary
            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA vi
Mu-like viruses.
NCBI_TaxID=10671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: AMP + H(2)0 = IMP + NH(3).

-!- PATHWAY: PURINE NUCLEOTIDE CYCLE.

-!- SUBSUNT: HOMOTESTRAMER.

-!- TISSUE SPECIFICITY: THREE ISOFORMS ARE PRESENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMPDI
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=87316928; PubMed=2957646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteriophage D108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNIV_BPD10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase; Nucleotide metabolism; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isoform M) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MNQKHLLRFI KKSYQVDADR VVYSTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: THREE ISOFORMS ARE PRESENT IN MAMMALS: AMP DEAMINASE 1 IS THE PREDOMINANT FORM IN SKELETAL MUSCLE; AMP DEAMINASE 2 PREDOMINATES IN SMOOTH MUSCLE, NON-MUSCLE TISSUE, EMBRYONIC MUSCLE AND UNDIFFERENTIATED MYOBLASTS; AMP DEAMINASE IS FOUND IN ERYTHROCYTES.
SIMILARITY: BELONGS TO THE ADENOSINE AND AMP DEAMINASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS00485; A_DEAMINASE; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR001365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cuniculus (Rabbit).
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          December 22, 2002 19:30 Type: P Check: 7826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3169 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A/AMP_deaminase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B022467EACBB6E75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 AA
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                                                                                            restrictions
                                                                                                                    EMBL outstation
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   FIBB_ANTAM Length: 21
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Blomback B., Blomback M., Grondahl N.J.;
"Studies on fibrinopeptides from mammals.";
acta Chem. Scand. 19:1789-1791(1965).
-i- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 1.0
                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                               01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Fibrinogen beta chain (Contains: Fibrinopeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEPTIDE MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arch.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1990 (Rel. 13, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P14465;
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PROSITE; PS00397; RECOMBINASES_1; PARTIAL.

PROSITE; PS00398; RECOMBINASES_2; PARTIAL.
                                                                                                                                  Bovidae; Bovinae; Bison.
                                                                                                                                                                                  Bison bonasus (European bison).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antilocapridae;
                                                                                       SEQUENCE
                                                                                                                    NCBI_TaxID=9902;
                                                                                                                                                                                                                                                                                     P14466;
                                                                                                                                                                                                                                                                                                   FIBB_BISBO
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                              MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blood coagulation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mross G.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ب
                                                                                                                                                                                                                                                                                                                                                 1 QPSYDYDEEE DDRAKLRLDA R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS. MISCELLANEOUS: CONVERSION OF FIBRINGGEN TOFFIRNIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. SITE: FIbringen_C.

SITE: PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
od coagulation; Plasma; Sulfation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ino acid sequence studies on artiodacty fibrinopeptides.";
h. Blochem. Blophys. 122:674-684(1967).
FUNCTION: FIBRINGGEN HAS A DOUBLE FUNCTION: YIELDING MONOME
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGREGATION
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                                                                                                                                                                                                                                                                                                                                                                                                              21 AA;
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                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                              2585 MW;
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097E607032767C38 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SULFATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIBRINOPEPTIDE B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                              2002 19:30 Type: P
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                                                                                                                                                                                                                                                                                                 AΑ
                                                                                                                                                                                                                 B] (Fragment).
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DA PAC

P14468; 01-JNA1990 (Rel. 13, Created) 01-FEB-1994 (Rel. 28, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) !!AA\_SEQUENCE 1.0

FIBB\_CEREL

STANDARD;

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FIBB_BISBO Length: 21
                             FIBB_BUBBU
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MOD_RES
NON_TER
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GUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
GLEHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

HISCELLANEOUS: CONVERSION OF FIBRINGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINGPETIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.

INTERPROJECTION OF THE SOFT CLOT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bubalus bubalis (Domestic water buffalo).
Eukaryota: Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1990 (Rel. 13, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 1.0
                                                            SEQUENCE
                                                                                                                                                                                                                                                             -
                                                                                                                                                                                                                                                                                                           Biochim. Biophys. Acta 405:517-521(1975).
                                                                                                                                                                                                                                                                                                                                                      STRAILN=Italian breed;
MEDLINE=76040091; PubMed=1180969;
Balestrier1 C., Colonna G., Irace G.;
"Covalent structure of fibrinopeptides from buffaloes breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mross G.A., Doolittle R.F.;
"Amino acid sequence studies on artiodacty fibrinopeptides.";
Arch. Blochem. Blophys. 122:674-684(1967).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                     InterPro; IPR002181; Fibrinc
PROSITE; PS00514; FIBRIN_AG_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
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                                                                                                                                       Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=89462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P14467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIBB_BUBBU
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                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                              SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS. MISCELLANEOUS: CONVERSION OF FIBRINGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE NOTERNINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
                                                                                                                                                                                                                                                                               AGGREGATION.
                                                                                                                                                                                                                                                                                             POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
QFPTDYDEGQ DDRPKLGLGA R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFPTDYDEGE DDRPKVGLGA R
                           Length: 21
                                                                                                                                       coagulation; Plasma; Sulfation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovinae; Bubalus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 AA;
                                                            21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               σH
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                             December 22,
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                                                            2379 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2366 MW;
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                                                                                                                                                     C_DOMAIN; PARTIAL.
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                                                            09EE75BE4729163D CRC64;
                                                                                                     FIBRINOPEPTIDE B.
PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09EE75AF19E6363D CRC64;
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                                                                                           SULFATION.
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                             2002 19:30
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                             Type: P
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                             Check: 7185
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FIBB_CEREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mross G.A., Doolittle R.F.;

"Amino acid sequence studies on artiodacty fibrinopeptides.";

Arch. Biochem. Biophys. 122:674-684(1967).

-I- FUNCTION: FIBRINGEN HAS A DOUBLE FUNCTION: YIELDING MONO
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Studies on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=C.e.nelsoni;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=C.elaphus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9860,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cervus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fibrinogen FGB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acta Chem.
                                                                                                                                                                                                                                                                                                                            01-JAN-1990 (Rel. 13, 01-JAN-1990 (Rel. 13, 15-JUN-2002 (Rel. 41,
PEPTIDE NON_TER
                                                                                                                                                                                                                                                             Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blood coagulation;
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                                                                                                                                                                                                                                                                                                                  Fibrinogen beta
                          Blood
                                                                                                                                                                 "Studies on fibrinopeptides from mammals.", Acta Chem. Scand. 19:1789-1791(1965).
-I FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCT
                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                 NCBI_TaxID=9685;
                                                InterPro;
                                                                                                                                                                                                            Blomback
                                                                                                                                                                                                                                                                                                                                                                                    IBB_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 (ALPHA, BETA AND GAMMA), LINKED TO EACH MISCELLANEOUS: CONVERSION OF FIBRINOGEN THROMBIN, WHICH CLEAVES FIBRINOPETIDES CHAINS, AND THUS EXPOSES THE N-TERMINAL
                                                                       SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS. MISCELLANGOUS: CONVERSION OF FIBRINGEN TO FIBRIN IS TRIGGREED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETY CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. PPRO02181; Fibrinogen_C. TPRO02181; FIBRIN_AG_C_DOMAIN; PARTIAL.
                                    RESPONSIBLE FOR THE FORMATION OF THE SOFT PROPOSED FOR THE FORMATION OF THE SOFT SITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
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                                                                                                                                            AGGREGATION
                                                                                                                                                         POLYMERIZE INTO FIBRIN AND
                                                                                                                                                                                                                                                                                                                                                                                  FELCA
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                         coagulation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n fibrinopeptides from mammals."; scand. 19:1789-1791(1965).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blomback M.,
                                                                                                                                                                                                            Blomback M.,
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azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Red deer),
                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                          Plasma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW.
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                                                                                                                                                                                                            Grondahl N.J.;
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                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                          DOUBLE
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                                                                                                                                                         FUNCTION: YIELDING MONOMERS THAT AS A COFACTOR IN PLATELET
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                                                                 SOFT CLOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER BY DISULFIDE BOND TO FIBRIN IS TRIGGERED A AND B FROM ALPHA & BE POLYMERIZATION SITES
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                                                                                                                                                                                                                                                                   Futeleostomi;
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                                                                                           ED BY
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FIBB_FELCA Length:
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  OCCOS GET TTACE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blomback B., Blomback M., Grondahl N., "Studies on fibrinopeptides from mammus Acta Chem. Scand. 19:1789-1791(1965).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1990
01-JAN-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=L.glama;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Camelus dromedarius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FGB
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Eukaryota;
Mammalia; E
Cervidae; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=C.dromedarius;
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                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3
(ALPHA, BETA AND GAMMA), LINKED TO EACH
-!- MISCELLANEOUS: CONVERSION OF FIBRINGEN
THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=67209145; PubMed=6033721;
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                                                                                                                          01-JAN-1990 (Rel. 13,
01-FEB-1994 (Rel. 28,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=L.vicugna;
Mross G.A., Doolit
                                                                                                                                                                                           P14475;
                                                                                                                                                                                                        FIBB_MUNMU
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                            PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE.
                                                            Muntiacus muntjak
                                                                                                    Fibrinogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ino acid sequence studies on artiodacty fibrinopeptides.";
h. Biochem. Biophys. 122:674-684(1967).
FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOME
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glama (Llama),
vicugna (Vicugna)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGREGATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IIDYYDEGEE
                                                                                                                                                                                                                                                                             ATDYDEEEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                              coagulation;
                                                                                                                                                                                                                                                                                                                   Length: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; IPR002181; Fibrinogen_C.
PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gna (Vicugna) (Vicugna vicugna), and romedarius (Dromedary) (Arabian camel). romedarius (Dromedara; Craniata; Vertebrata; Butheria; Cetartiodactyla; Tylopoda; Came
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                      Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Cetartiodactyla; Ruminantia; Pec
    Muntiacinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel.
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                                                                                                        beta
                                                                                                                                                                                                                                                                                                                                                                19 AA;
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                                                                                                                                                                                                                                                                           RVKVRLDAR
                                                                                                           chain
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                                                                (Muntjak).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2328 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasma; Sulfation
                                                                                                                                                                                                                                                                                                                        December
                                                                                                                                                                                                                                                                                                                                                                2295
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Last annotation update)
[Contains: Fibrinopeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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Last annotation update)
[Contains: Fibrinopeptide
                                                                                                                                                                                                                                                                                                                                                                MW;
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                                                                                                                                                                                                                                                                                                                        22,
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                                                                                                                                                                                                                                                                                                                                                                                                          SULFATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                 FIBRINOPEPTIDE
                                                                                                                                                                                                                   PRT;
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mammals.";
                                                                                                                                                                                                                                                                                                                          19:30
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                                                                                                                                                                                                                   AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NONIDENTICAL CHAINS
OTHER BY DISULFIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Camelidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YIELDING MONOMERS
                                                                                                             B] (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Check: 5816
                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                          Check: 4317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IS TRIGGERED BY
'M ALPHA & PTT
                             Cervoidea;
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SQUE TENT
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                            !!AA_SEQUENCE 1.0
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                                                                                                                                    PEPTIDE
MOD_RES
MOD_RES
NON_TER
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"Amino acid sequence studies on artiodactyl fibrinopeptides. I.
Dromedary camel, mule deer, and cape buffalo.";
Arch. Biochem. Biophys. 118.456-467(1967).
-i- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Cet
Cervidae; Odocoileinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FGB.
Odocoileus hemionus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEPTIDE
MOD_RES
MOD_RES
NON_TER
   P14479;
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01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 1.0
                FIBB_
                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fibrinogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL Blood coagulation; Plasma; Sulfation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .<u>.</u>,
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                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=67209145; PubMed=6033721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9872;
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"Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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{1}
                                                                                                                                                                                                       SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS. MISCELLANBOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETT CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. CETPCO; LPRO02181; Fibrinogen_C.

SITE; P800514; FIBRIN_AG_C_DOMAIN; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS. MISCELLANBOUS: CONVERSION OF FIBRINGGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ino acid sequence studies on artiodacty fibrinopeptides.";

h. BioChem. Biophys. 122:674-684(1967).

EUNCTION: TIBRINGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGREGATION
                                                                                                                                                                                                                                                                                                                                  AGGREGATION.
                                                           QHLADYDEVD DDRAKLHLDA
                RANTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QHSTDYDEVE DDRAKLHLDA R
                                                                                                                                                                                               coagulation; Plasma; Sulfation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      beta chain [Contains: Fibrinopeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21
                                                                                                                       AA;
                                                                                        21
              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           December 22,
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                                                                                        December
                                                                                                                     2496 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Eutel
Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Mule deer) (Black-tailed deer).
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                                                                                                                     FCF562C51A0C1627 CRC64;
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                                                                                                                                                    SULFATION.
                                                                                                                                                                 PYRROLIDONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PYRROLIDONE
                                                                                                                                                                                 FIBRINOPEPTIDE
                PRT;
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                                                                                        2002 19:30
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                21
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                AΑ
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                                                                                                                                                                 CARBOXYLIC
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                                                                                      Type: P
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                                                                                                                                                                  ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                        Check: 6856
                                                                                                                                                                                                                                                                      TRIGGERED BY
ALPHA & BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cervoidea;
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FIBB_RANTA Length: 21
              PEPTIDE
MOD_RES
MOD_RES
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                                                                                                -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
-!- MISCELLANEOUS: CONVERSION OF FIBRINGEN TO FIBRIN IS TRIGGERED BY
THROMEIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
                                                                                                                                                                                                        Doolittle R.F., Schubert D., Schwartz S.A.;
"Amino acid sequence studies on artiodacty! fibrinopeptides. I.
"Dromedary came!, mule deer, and cape buffalo.";
Arch. Biochem. Biophys. 118:456-467(1967).
-i- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                     Syncerus caffer (Cape buffalo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISCULFIDE BONDS.
-!- MISCELLANBOUS: CONVERSION OF FIBRINGER TO FIBRIN IS TRIGGERED BY
THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
InterPro; IPRO02181; Fibrinogen_C.
InterPro; IPRO02181; Fibrinogen_C.
PROSSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rangifer tarandus (Reindeer) (Caribou).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1990 (Rel. 13,
01-FEB-1994 (Rel. 28,
15-JUN-2002 (Rel. 41,
Fibrinogen beta chain
                                                                                                                                                                                                                                                                                                                                          Bovidae; Bovinae;
NCBI_TaxID=9970;
                                                                                                                                                                                                                                                                                                                                                                                                                    FGB
                                                                                                                                                                                                                                                                                                                                                                                                                                   Fibrinogen beta
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1994 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P14481;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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 NON_TER
                                                            Blood
                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blood coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9870;
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                                                                         PROSITE;
                                                                                     InterPro;
                                                                                                                                                                                                                                                                                               MEDLINE=67209145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: FIBRINGEN HAS A DOUBLE FUNCTION: YIELDING POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PL
                                                                                                                                                                                              AGGREGATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QHLADYDEVE DDRAKLHLDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYNCA
                                                          coagulation;
                                                                     ; IPR002181; Fibrinogen_C. PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Odocoileinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ., Blomback M., Grondahl N.J.; n fibrinopeptides from mammals."; Scand. 19:1789-1791(1965).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                   chain
                                                                                                                                                                                                                                                                                                                                                                                                                                              13,
28,
41,
                                                                                                                                                                                                                                                                                               PubMed=6033721;
                                                                                                                                                                                                                                                                                                                                                          Syncerus.
Plasma;
21
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21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2510 MW;
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Last annotation update)
[Contains: Fibrinopeptide B] (Fragment)
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                            Sulfation
                          FIBRINOPEPTIDE B.
PYRROLIDONE CARBOXYLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                B] (Fragment).
                                                                                                                                                                                                                                                                                                                                                                        Pecora; Bovoidea;
                               ACID
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REAR RECEPTION OF THE RECEPTION OF TH
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
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01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Gef leader peptide.
GEFL OR B0018.
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PRINTS; PR00275; GJUCAGON,
SMARR: SM0070; GJUCAGON; 1.
PROSITE; PS00260; GJUCAGON; 1.
Glucagon family; Hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nguyen T.M., Wright J.R. Jr., Nielsen P.F., Conlon J.M.; "Characterization of the pancreatic hormones from the Brockmann body of the tilapia: implications for islet xenograft studies."; Comp. Biochem. Physiol. 111C:33-44(1995).
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Eukaryota, Metazoa. Chordata, Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
Cichiidae; Oreochromis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IN RESPONSE TO A DROP IN BLOOD SUGAR CONCEN-
-!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glucagon
                                                      MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE-92048481; PubMed=1943701;

Poulsen L.K., Refn A., Molin S., Andersson P.;

"The gef gene from Escherichia coli is regulated at the level of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000532; Glucagon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P01274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95384941; PubMed=7656183;
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                                                                                                                                                                                                                        SEQUENCE FROM N.A
STRAIN-K12 / MG16!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-8128;
"The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                     Mol. Microbiol. 5:1639-1648(1991).
                                                                                                                                                                                                                                                                                                                                                    translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 HSEGTFSNDY SKYLEDRKAQ DFVRWLMNNK RSGAAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . Biochem. Physiol. 111C:33-44(1995).
FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
THE BLOOD SUGAR LEVEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORENI
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                                                                                                                                                                                                                        MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4252 MW; SAAFBF0254425756 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUGAR CONCENTRATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 AA
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LPGE_ECOLI Length: 19 December 22, 2002 19:30 Type: P Check: 4518
MY14_EISFO Length: 14 December 22, 2002 19:30 Type: P Check: 7600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sanotation update)
Myoactive tetradecapeptide (ETP)
Myoactive tetradecapeptide (ETP)
Elsenia foetida (Common brandling worm) (Common dung-worm)
Elsenia foetida (Common brandling worm) (Common dung-worm)
Elsenia foetida (Limbricina; Limbricina; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EcoGene; EG12074; gefL.
Leader peptide; Complete proteome
SEQUENCE 19 AA; 2259 MW; 19B3
                                                                                                                                                                                                                                                                                                                                                                                                                           01-Nov-1995 (Rel. 32, Created)
01-Nov-1995 (Rel. 32, Last sequence update)
01-Nov-1995 (Rel. 32, Last annotation update)
01-Nov-1995 (Rel. 32, Last annotation update)
Myoactive tetradecapeptide (PTP).
Pheretima vittata (Barthworm).
Pheretima vittata (Barthworm).
Eukaryota: Metazoa; Annelida: Clitellata: Oligochaeta: Haplotaxida:
                                                     Peptides 16:995-999(1995).
-!- FUNCTION: HAS A STIMULATIVE EFFECT ON THE CONTRACTION OF GUT
                                                                                                                  "A novel gut tetradecapeptide isolated from the earthworm, Eisenia foetida.";
                                                                                                                                                                                                             MEDLINE-96087879; PubMed-8532604;
Ukena K., Oumi T., Matsushima O., Ikeda T., Fujita T., Minakata H.,
                                                                                                                                                                                                                                                                                                                                                              unimpricina; Megascolecidae; Pheretima.
NCBI_TaxID=46674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 14 AA; 1478 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neuropeptide; Amidation. MOD_RES 14 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A novel gut tetradecapeptide isolated from the earthworm, Eisenia foetida.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-96087879; PubMed-8532604;
Ukena K., Oumi T., Matsushima O., Ikeda T., Fujita T., Minakata H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MY14_EISFO
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   -!- SIMILARITY: TO INSECTS ALLATOTROPIN
                                                                                                                                                                                                                                                                                                             SEQUENCE, AND SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: TO INSECTS ALLATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID~6396;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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CC9ABEF941CD91AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19B3EDF371EB0BEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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I:AA_SEQUENCE 1.0

ID T2B_PARTE STANDARD; PRT; 23 AA.

AC Q27174;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 16-CCT-2001 (Rel. 40, Last annotation update)

DE Trichocyst matrix protein T2-B (Secretory granule protein T2-B)

DE (TMP 2-B) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SUBCELLULAR LOCATION: TRICHOCYST. THESE ARE ARCHITECTURALLY COMPLEX SECRETORY STORAGE GRANULES-DOCKED AT THE PLASMA MEMBRANE, READY TO RAPEDLY RESPOND TO AN EXOCYTOTIC STIMULUS.

1- SIMILARITY: BELONGS TO THE TMP FAMILY.

1- DATMARSE: NAME-POTCEIN Spotlight;
NOTE-ISSUE 3 of October 2000;
WMW-"http://www.expasy.org/spotlight/articles/spt1t003.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-95119139; PubMed-7819344; Maddeddu L., Gautier M.-C., le Caer J.P., de Loubresse N., Sperling L.; "Protein processing and morphogenesis of secretory granules in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUI-1999 (Rel. 38, Created)
15-JUI-1999 (Rel. 38, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Trichocyst matrix protein T2-A (Secretory granule protein T2-A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U27509; AAA92609.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Madeddu L., Gautier M.-C., Vayssie L., Houari A., Sperling L., "A large multigene family codes for the polypeptides of the Crystalline trichocyst matrix in Parameclum."; Mol. Biol. Cell 6:649-659(1995),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polyprotein; Structural protein; Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=5888;
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Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 14 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2720 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08972B1F2759BDB7 CRC64;
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DA40BEE67CCD91AD CRC64;
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T2B_PARTE Length: 23 December 22, 2002 19:30 Type: P Check: 1016
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                                                                                                                                                                                            Q92G33 PRELIMINARY; PRI; 2, ....
Q92G33;
Q1-MAY-1999 (TrEMBLrel. 10, Created)
Q1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
Q1-MAY-1999 (TrEMBLrel. 10, Last annotation update)
Subtilisin/chymotrypsin inhibitor (Fragment).
Chiamydia trachomatis.
Bacteria, Chiamydiales; Chiamydiaceae; Chiamydia.
                   EMBL; AF NON_TER NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  SEQUENCE
                                                                      sequencing.
Submitted (
                                                                                                       Wang L., Steenburg S.D., Zheng Y., Larsen S.H.; "Gene identification of Chlamydia trachomatis by random DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRICHOCYST MATRIX.

-!- SUBCELLULAR LOCATION: TRICHOCYST. THESE ARE ARCHITECTURALLY COMPLEX SECRETORY STORAGE GRANULES-DOCKED AT THE PLASMA MEMBRANE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochimie 76:329-335(1994).
-i- FUNCTION: STRUCTURAL PROTEIN THAT CRYSTALLIZE INSIDE THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDILINE-96059477; PubMed-7579685; Madeddu L., Gautier M.-C., Vayssie L., Houari A., Sperling L.; Madeddu L. fautier M.-C., Vayssie t., Houari A., Sperling L.; "A large multigene family codes for the polypeptides of the crystalline trichocyst matrix in paramecium."; mol. Biol. Cell 6:649-659(1995).
                                                                                                                                              STRAIN=L2 434B;
                                                                                                                                                                SEQUENCE FROM N.A.
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--- SIMILARITY: BELONGS TO THE TWP FAMILY.
--- DATABASE: NAME-Protein Spotlight;
NOTE-Issue 3 of October 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Madeddu L., Gautier M.-C., le Caer J.P., de Loubresse N., Sp
"Protein processing and morphogenesis of secretory granules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Paramecium tetraurelia.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
Paramecium
NCBI_TaxID=5888;
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                                       tted (AUG-1998) to the EMBL/GenBank/DDBJ databases. AF087336; AAD14110.1; -. _{\rm ER}
17 AA; 2043 MW;
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Q9ZG33 Length: 17 December 22, 2002 19:30

Type: P Check: 1658

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!!AA_SEQUENCE 1.0
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O1-OCT-2000 (TrEMBLrel. :
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O1-OCT-2000 (TrEMBLrel. :
F81r (Fragment).
       J. Bacter101. 179:7784-7789(1997).
EMBL; AJ243803; CAB50742.1; -
InterPro; IPR001825; NTP_transferase.
Pfam; PF00483; NTP_transferase; 1.
NON_TER 25 25
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01-NOV-1999 (TrEMBLrel.
01-UN-2002 (TrEMBLrel.
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Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF230491; AAF82664.1; -.
NON_TER 24 24
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; St
                                                                                                                                                                                                                        Martin M., Schneider D., Bruton C.J., Chater "A 919C Gene Essential Only for the First of Phases of Glycogen Synthesis in Streptomyces J. Bacteriol 179:7784-7789(1997).
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cterium group; Methylobacterium
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Two Spatially Distinct
coelicolor A3(2).";
          Rhizobiaceae
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01-NOV-1996
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KATG.
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                                                                                                                      Cockerill F.R., Uhl J.R., Temesgen Z., Zhang Roberts G.D., Williams D.L., Kline B.C.; "Rapid Identification of a point mutation of tuberculosis catalase-peroxidase (katG) gene resistance.";
                                                                                                                                                                                                                                                                                                                                                                                                                     Bergh S.T., Uhlen M.;
"Cloning, analysis and heterologous expression synthesis genes of Streptomyces curacoi.";
Submitted (JUN-1990) to the EMBL/GenBank/DDBJ (EMBL; M33704; AAA26724.1; -.
NON_TER 1
                                                                                      Submitted (FEB-1994) to the EMBL/GenBank/DDBJ EMBL; U06263; AAB59976.1; -. SEQUENCE 13 AA; 1564 MW; 2F39A45EFE994777
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EMBL: L41608; AAA85567.1;
                                                                                                                                                                               STRAIN-L10373;
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                              Actinomycetales;
NCBI_TaxID=1773;
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Submitted (SEP-2001) to the EMBL; AJ413194; CAC88360.1; NON_TER 1
                                                                     Levican G., Bruscella
Bonnefoy V., Holmes D.
"Characterization of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUL-2001) to the EMBL; AJ311888; CAC44744.1;
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Bruscella P., Lev
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Bacteria; Firmicutes; Actinobacteria
Actinomycetales; Corynebacterineae;
                                                                                                                            STRAIN-ATCC33020;
                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                Thiobacillus ferrooxidans Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A second operon encoding ferrooxidans.";
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homologous recombination.";
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                                                        ferrooxidans.";
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BL; U92075; AAB71427.1; -.
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homolog essential for photochromogenicity in Mycobacterium
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Alpha-acceptor polypeptide M15 (Fragment)
Escherichia coli.
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Q9NZ25;
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SEQUENCE FROM N.A.
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Submitted (DEC-1999) to t
EMBL; AF220215; AAF67661.
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Eukaryota; Metazoa; (
Mammalia; Eutheria; I
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Infect. Immun. 58:2651-2658(1991).
EMBL; M64295; AAA27272.1; -.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Phosphoribosylpyrophosphate synthetase isoform I (Fragment).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAY-2000 (TrEMBLrel. 13, Last annotation update)
Phosphoribosylpyrophosphate synthetase isoform II (Fragment).
Homo sapiens (Human)
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isoforms.";
Biochim. Biophys. Acta 1130:139-148(1992).
EMBL; D28134; BAA05676.1; -.
                                                                                                                                               MEDLINE-92233087; PubMed=1314091; Ishiyima S., Sonoda T., Shimada H., Ishiyuka T., Iizasa T., Taira M., Ishijima S., Sonoda T., Shimada H., Nagatake N., Tatibana M.; Promoter regions of the human X-linked housekeeping genes pRPS1 and "PRPS2 encoding phosphoribosylpyrophosphate synthetase subunit I and I
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Nagatake N., Tatibana M.;
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2282 MW;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last anno
Tropomyosin (Fragment).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
L-isoaspartyl/D-aspartyl methyltransferase (Fragment).
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                                                        096F68;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                      pathogenetic mechanism for ulcerative colitis.
J. Immunol. 150:2487-2493(1993).
InterProj. IPRO00533; Tropomyosin.
Pfam; PF00261; Tropomyosin; 1.
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        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                         SEQUENCE
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                                           Unknown (Protein for IMAGE: 4563468) (Fragment).
                                                                                                                                                                                                                                                                                                                              MEDLINE=93195352; PubMed=8450225;
                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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PF01135; PCMT; 1.
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S73902; AAC60639.2; -
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                                                                                                                                                                                                                         Tropomyosin;
AA; 1802 MW;
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Last annotation updat
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                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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!!AA_SEQUENCE 1.0
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                             Q9GU45
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                                                                         NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stretchin-MLCK (Fragment).

STRN-MLCK OR CG8304 OR CG18255.

Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Pthygota; Drosophilidae; Drosophila.
                                                                                                                    Mol. Phylogenet. Evol. 17:97-107(2000).
EMBL; AF197140; AAG28510.1; -.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chain Kinase Family.";
J. Mol. Biol. 0:0-0(2000).
EMBL; AF557309; ARF90127.1;
ELYBase; FB9n0013988; Strn-Mlck.
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC01156; AAH11555.1; -.
NON_TER 1 1
                                                                                                                                                                                                   Manuel M.,
                                                                                                                                                                                                                                                                NCBI_TaxID=56443;
                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                Sycon raphanus
                                                                                                                                                                                                                                                                                                                               SYCOX2
                                                                                                                                                                                                                                                                                                                                           Homeobox protein Sycox2
                                                                                                                                                                                                                                                                                                                                                                                                           Q9GU45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Champagne M.B., Edwards K.A., Erickson H.P., Kiehart D.P.;
"Drosophila stretchin-MLCK is a Novel Member of the Titin/Myosin Light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 28 AA; 2841 MW; 5799D138245D3951 CRC64;
                                                             SEQUENCE
                                                                                                            Pfam;
                                                                                                                                                                      raphanus."
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=20476455; PubMed=11020308;
                                                                                                                                                                                                                                                                                    Sycettidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
{1}
                                                                                                                                                                                    "Homeobox Gene Diversification in the Calcareous Sponge, Sycon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7227;
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                             Length: 27 December 22, 2002 19:30
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KTSKYLAPTT RQALAARLGL TDRQVKV
                                                                                                       PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 AA; 3004 MW; 2F2CB3A55E7FF033 CRC64;
                                                          27 AA;
                                                                                                                                                                                                   Le Parco Y.
                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                            2986 MW;
                                                                                                                                                                                                                                                                                              Porifera; Calcarea;
                                                                                                                                                                                                                                                                                                                                             16, Created)
16, Last sequence update)
17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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                                                        CA58FA11B629E3B7 CRC64;
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                                                                                                                                                                                                                                                                                             Calcaronea; Leucosoleniida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Type: P Check: 6662
                           Type: P Check: 9325
                                                                                                                                                                                                                                                                                                                                                                                                                         AA.
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PARSON (TREMBLIEL 16, Created).
01-MAR-2001 (TREMBLIEL 16, Last sequence update)
01-MAR-2001 (TREMBLIEL 17, Last annotation update)
01-JUN-2001 (TREMBLIEL 17, Last annotation update)
The protein Sycox3 (Fragment).
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!!AA\_SEQUENCE 1.0

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Q94681;
Q94681;
Q1-FEB-1997 (TrEMBLrel. 02, C
01-FEB-1997 (TrEMBLrel. 02, L
01-JUN-2001 (TrEMBLrel. 17, L
PMHDOX1 (Fragment).
          STRAIN-USHIMADO;
FUjiwara S., Kawamura K.;
"Cloning of homeobox-containing genes
                                                                                                                                                                                                                                                                                                      SEQUENCE 1.0
                                                                                                          Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Stolidobranchia; Styelidae; Polyandrocarpa. NCBI_TaxID=7723;
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last seq
01-NOV-1999 (TrEMBLrel. 12, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
NON_TER 1 1
NON_TER 27 27
Polyandrocarpa misakiensis.";
                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                    Polyandrocarpa misakiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilding C.S., Grahame J., Mill P.J.;
"Molecular characterisation of calmodulin intron variation
Littorina (Gastropoda: Prosobranchia) species.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Littorina saxatilis.
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Mesogastropoda; Littorinoidea; Littorinidae; Littorina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Calmodulin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sycon raphanus.
Eukaryota; Metazoa; Porifera; Calcarea; Calcaronea; Leucosoleniida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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"Homeobox Gene Diversification in the Calcareous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ133335; CAB44224.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=31220;
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EMBL; AF197141; AAG28511.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=20476455; PubMed=11020308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sycettidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     raphanus."
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27 27
27 AA; 3014 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                       23 AA; 2815 MW;
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Last annotation updat
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                       5762B9C4E9886A06 CRC64;
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                                                                                                                                                                                                                                                                                     PRT;
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                from the budding ascidian
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                                                                                                                                                                                                          update)
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  Q25482
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                                                                                                                                                                                                                                                                                                                                                                                                                   Metridium senile (Brown sea anemone) (Frilled sea anemone).
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinia
Nynantheae; Metridiidae; Metridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TREMBLIEGL 01, 01-NOV-1996 (TREMBLIEGL 01, 01-DEC-2001 (TREMBLIEGL 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dick M.H., Buss L.W.;
Submitted (MAY-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ctenodrilus serratus.
                                                     SEQUENCE
                                                                                                                                                                                                 EMBL; U42727; AAA86626.1;
                                                                                                                                                                                                                       Nematostella vectensis and Metridium senile.", Biol. Bull. 193:62-76(1997).
                                                                                                                                                                                                                                                                      Finnerty J.R., Martindale M.Q.; "Homeoboxes in sea anemones (Chidaria:Anthozoa): a
                                                                                                                                                                                                                                                                                                                            MEDLINE-97435515; PubMed-9290214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anthox1.Ms (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A PCR-based survey of homeobox genes in Ctenodrilus serratus (Annelida: Polychaeta).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=94356262; PubMed=7915607;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
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                                                                                                  NON_TER
                                                                                                                                                  InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
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                                                                                                                               PRINTS;
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     Length:
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D88274; BAA13570.1; -.
pr001356; Hommobox.
                                                                                                                            PR00024; HOMEOBOX.
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                                                  27 AA;
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     December 22,
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                                                  3314 MW;
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Last annotation update)
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Last annotation update)
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     2002 19:30
                                                     E6B0D191EE3905CF CRC64;
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Irvine S.M., Warinner S.A., Hunter J.D., Martindale M.Q.;
"A survey of homeobox genes in Chaetopterus variopedatus
of polychaete homeodomains.";
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U68283; AAB16992.1; -.
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                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Crustacea; Rhizocephala; Kentrogonida; Sacculinidae; S
                                                                                                                                                                                                                                                                                                                                                                                                                                     Caudal (Fragment).
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Spionida; Chaetopteridae; Chaetopterus.
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SEQUENCE FROM N.A.
                      NCBI_TaxID=10201;
                               Eukaryota; Metazoa; Ctenophora; Cyclocoela; Beroida;
                                            Beroe ovata.
                                                                               01-MAY-1997
                                                                                          01-MAY-1997
                                                                                                         P91901;
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Pfam; PF00046; homeobox; 1.
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EMBL; U79471; AAD00342.1; -
                                                                                                                                                                                                                                                                                                                         MEDLINE=98334561; PubMed=9667986; Mouchel-Vielh E., Rigolot C., Gib
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=51650;
                                                                                                                                                                                                                                                                                                                                                                                                             Sacculina carcini
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                                                       Homeobox protein
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27 AA;
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                                                                                                                                                                                                                                                 ESCRIVA H., Safi R., Hanni C., Langlois M.C., Saumitou-Laprade P., Stehelin D., Capron A., Pierce R., Laudet V.; "Ligand binding was acquired during evolution of nuclear receptors."; Proc. Natl. Acad. Sci. U.S.A. 94:6803-6808(1997).

PROC. Natl. Acad. Sci. U.S.A. 94:6803-6808(1997).
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01-JAN-1998 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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"BHOX35 - Beroe Homeobox.";
BHOX35 - Beroe Homeobox.";
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U89383; AAB49473.1; -.
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Pfam; PF00046; homeobox; 1.
                                                                        DNA-binding; Nuclear
                                                                                                    SMART;
                                                                                                                             ProDom;
                                                                                                                                                      Pfam; PF00105;
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                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=97338099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Artemia salina (Brine shrimp)
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                                                                                                                                                                         InterPro; IPR001628; Znf_C4steroid.
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                                                  finger.
                                                                                              PF00105; zf-C4; 1.
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SM00399; ZnF_C4; 1.
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RA Beeson K.Y. Benos P.V. Berman B.P. Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeywam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Woshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Woshrefi A.,
RA Reinert K.M., Remington K.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Winskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Zheng X.H., Zhong F.N., Zhong M., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong M., Zhou S., Zhu X., Smith H.O.,
RA Zheng X.H., Shori S., Ra M., Koologe T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong M., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong M., Zhong M., Venter J.C.,
RT Typerson Sequence of Drosophila melanogaster.";
DR EMBL; Ascological Acc., Carlads S.
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                                                                             !!AA_SEQUENCE 1.0
                                                                                                                                                                           Q9V973 Length: 17
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01-MAY-2000
01-MAY-2000
Q9TWR1;
01-MAY-2000 (TrEMBLrel, 13, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                         Q9TWR1
                                                                                                                                                                                                                               FlyBase; FBgn0034547;
SEQUENCE 17 AA; 19
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NCBI_TaxID=7227;
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01-MAY-2000 (TrEMBLrel.
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                                                                                                                                                                        2002 19:30 Type: P Check: 1645
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01-AUG-1998
01-MAR-2002
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MEDLINE=94086476; PubMed=8262908;

MEDLINE=94086476; PubMed=8262908;

Takahashi S.Y. Yamamoto Y. Shionoya Y., Kageyama T.;

Toysteine proteinase from the eggs of the silkmoth, Bom 
"Cysteine proteinase from the eggs of the silkmoth, Bom 
"dentification of a latent enzyme and characterization 
and proteolytic processing in vivo and in vitro.";

J. Blochem. 114:267-272(1993).

SECULTRICAL STATES AND STATES
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Bombyx mori (Silk moth).
Bukaryota; Metazoa; Arthropoda; Trac
Eukaryota; Neoptera; Endopterygota;
Bombycoidea; Bombycidae; Bombyx.
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                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
HOX11-D125 protein (D125) (Fragment).
HOX11-D125 OR D125.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Dterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98196665; PubMed-9537319; MEDLINE-98196665; PubMed-9537319; Canning E.U., Okamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            062575;
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Eukaryota; Metazoa; Myx
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   Dear T.N., Sanchez-Garcia I., Rabbitts T.H.; "The HOX11 gene encodes a DNA-binding nuclear transcription belonging to a distinct family of homeobox genes."; Proc. Natl. Acad. Sci. U.S.A. 90:4431-4435(1993). EMBL; L08618; AAA28612.1; -.
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OR MYX4.
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IIAA_SEQUENCE 1.0
ID Q9MZW8
AC Q9MZW8;
DT 01-OCT-2000 (7)
DT 01-OCT-2000 (7)
DT 01-OCT-2000 (7)
DE Von willebranc
OS Pongo pygmaeus
OC Eukaryota; Mei
OC Mammalia; Eutl
OC Mammalia; TaxID=960
RN [1]
RN [1]
RP SEQUENCE FROM
RX MEDLINE=20072;
RAA GOOdman M.;
RT The place of
RI tree: evidence
RL Mol. Phylogen
DR EMBL; AF09283
FT NON_TER
FT NON_TER
SQ SEQUENCE 29
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ID Q29394
   AC
DT
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InterPro; IPR001356; Homeobox.
Pfam; PF000046; homeobox; 1.
ProDom; PD000010; Homeobox; 1.
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01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
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Q9TRS7
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Mol. Phylogenet. Evol. 13:3
EMBL; AF092833; AAF77601.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pongo pygmaeus (Orangutan).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Von Willebrand
                                                                                                                                                                                                                                                                                   Receptor.
NON_TER
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Biochem Corre
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Mammalia; Eutheria;
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Q9TRS7;
01-MAY-2000
                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                       EMBL; L77673; AAA97423.1;
                                                                                                                                                                                                                                                                                                                                                                                                         Biochem.
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n Willebrand factor gene intron II sequence:
13:392-404(1999).
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
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MEDLINE=96061967; PubMed=7588764; Cho S.W., Lee J., Choi S.Y.;
                                                   Bovidae; Bovinae;
NCBI_TaxID=9913;
                                                                               Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                  "A novel glutamate dehydrogenase from bovine brain: characterization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2000 (TrEMBLrel. 14, Last annotation update)
Glutamate dehydrogenase isoform I (EC 1.4.1.2) (Fragment).
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01-JUN-2002 (TrEMBLrel.
Vitronectin (Fragment).
                                                                                                                                                                                                          SEQUENCE 1.0
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                             SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                  Lee
                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96043916;
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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AA; 1754 MW;
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MW; 65F7CD91023AEEBA CRC64;
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J. Biochem. 7
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01-NOV-1996
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
VAMP/synaptobrevin-2 (Fragment).
Sugiura M.; "Loss of all ndh genes as chloroplast genome of the
                                                                                                                                                                                                          Tsudzuki J., Nakashima K., Tsudzuki T., H
wakasugi T., Sugiura M.;
"Chloroplast DNA of black pine retains a
lacking rRNA genes: nucleotide sequences
trnH and the absence of rps16.";
                                                                                                                    MEDLINE-95094312; pubMed-8001170;
Tsudzuki J., Ito S., Tsudzuki T., Wakasugi T., Sugiura M.;
Ta naw gene encoding trNA(Pro) (GGG) is present in the chloroplast
genome of black pine: a compilation of 32 tRNA genes from black pin
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
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Horikawa H.P., Saisu H., Ishizuka
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                                          Wakasugi T.,
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MEDLINE=95024047; PubMed=7937893;
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                                        Tsudzuki J., Ito S., Nakashima K., Tsudzuki T.,
                                                                                              26:153-158(1994)
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  determined by sequencing the black pine Pinus thunbergii.
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Last sequence up
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Pinus.
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01-DEC-2001
01-DEC-2001
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"Chloroplast-encoded chlB is required for light-independent protochlorophyllide reductase activity in Chlamydomonas reinhardtii.";
plant Cell 5:1817-1829(193).
EMBL; D17510; BAA04307.1; -.
EMBL; D11467; BAA02023.1; -.
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Chloroplast.
22 AA;
                                        "Sequence analysis of chosen regions Pinus mugo and P. sylvestris."; Submitted (MAR-2001) to the EMBL/Geni
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Ribosomal protein S12 (Fragment).
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         Mitochondrion.
                                                                          SEQUENCE FROM N.A.
Wachowiak W., Liepelt S.,
                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; NCBI_TaxID=28528;
                                                                                                                                                      Pinus mugo
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                                                                                                                                                                                                                                                                                                                                                                                          Liepelt
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                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia. NCBI_TaxID=3562;
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"Acyl-(acyl-carrier protein) hydrolase from squash or
to long-chain fatty acids: purification and characte:
Plant Mol. Biol. 20:199-206(1992).
SEQUENCE 20 AA; 1973 MW; AE5304F9CD73D36E CRC64;
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01-JUN-2000 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3662;
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es; Pinaceae;
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MEDLINE-95394976; PubMed=7665625;

RYAD M.T., Naylor D.J., Hoogenraad N.J., Hoj P.B.;

J. Biol. Chem. 270:22037-22043(1995).

PROFIDENCE 24 AA; 2642 MW; B797841E1005A51A CRC64;
                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
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01-NOV-1996 (TIEMBLIEL 01, Last sequence update)
01-NOV-1996 (TIEMBLIEL 21, Last annotation update)
01-JUN-2002 (TIEMBLIEL 21, Last annotation update)
Ubiquitin conjugating enzyme UBC10 (Fragment).
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 Genomic DNA,
                           01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                               Desprez T., Amselem J., Chiapello H., Caboche M., Hofte H.; Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases. EMBL, Z29145; CAA82396.1; -. HSSP; P15731; 1QCQ.
                                                                                                                                                                                                                                                                                   STRAIN-CV. COLUMBIA; TISSUE-SEEDLING;
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                01-MAR-2001
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                                                                                                                                                                28 AA; 3321 MW;
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  chromosome
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16, Created)
16, Last sequence update)
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Q39633;
Q1-NOV-1996 (
                                                                                       Yamaguchi K., Subramanian A.R.;
"The plastid ribosomal proteins. Identification of all the proteins the 50 S subunit of an organelle ribosome (chloroplast).";
J. Biol. Chem. 275:28466-28482(2000).
-!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 55 RIBOSOMAL RNA.
-!- SUBCELLULAR LOCATION: CHLOROPLAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      p82195;
01-JUN-2000 (TrEMBLrel. 14, Created)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Chloroplast 50S ribosomal protein L18 beta (Fragment).
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MEDLINE-96104306; PubMed-8564304;
TOyama T., Teramoto H., Takeba G., Tsuji H.;
TOyama T., Teramoto H., Takeba G., Tsuji H.;
"Cytokinin induces a rapid decrease in the levels of mRNAs f catalase, 3-hydroxy-3-methylglutary! COA reductase, lectin a unidentified proteins in etiolated cotyledons of cucumber.";
Plant Cell physiol. 36:1349-1359(1995).
EMBL; D63385; BAA09701.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
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Cucumis sativus (Cucumber).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
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-!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
-!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 11.5 KDA.
-!- SIMILARITY: BELONGS TO THE L18P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                             STRAIN=CV. ALWARO; TISSUE=LEAF; MEDLINE=20435798; PubMed=10874046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spinacia oleracea (Spinach)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ databases.
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                           P83089 Length: 19
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                                                                                                                                                                                                                                                               Spinacia oleracea (Spinach).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Epermatophyta; Magnollophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.

NCBI_TaxID=3562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20435798; PubMed=10874046; Yamaguchi K., Subramanian A.R.; "The plastid ribosomal proteins. Identification of all the proteins the 50 S subunit of an organelle ribosome (chloroplast)."; biol. Chem. 275:28466-28402(2000).
-i- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 55 RIBOSOMAL RNA.
-i- SUBCELLULAR LOCATION: CHLOROPLAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spinacia oleracea (Spinach)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 1
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NON_TER 26
SEQUENCE 26 AA;
                                                                                      -!- SUBCELLULAR LOCATION: CHLOROPLAST; WITHIN -!- MASS SPECTROMETRY: MW=25300; METHOD=MALDI. Chloroplast; Thylakoid.
                                                                                                                                                                                                                                                                                                                                                           01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 1.0
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                                                           SEQUENCE
                                                                                                                                                                     Schubert M., Petersson U.A., Haas B.J., Funk C., Schroeder W.P., Kieselbach T.,
                                                                                                                                                                                                       PubMed=11719511;
                                                                                                                                                                                                                                    SEQUENCE,
                                                                                                                                                                                                                                                                                                                                            Thylakoid lumenal 25.3 kDa protein (Fragment)
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-!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 11.5 KDA.
-!- SIMILARITY: BELONGS TO THE L18P FAMILY OF RIBOSOMAL
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                                                                                                                       "Proteome map of the chloroplast lumen of Arabidopsis thaliana.";
J. Biol. Chem. 277:8354-8365(2002).
-!- SUBCELLULAR LOCATION: CHLOROPLAST; WITHIN THE THYLAKOID LUMEN.
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AIANAPLLDT TITDRVFFD
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                                                           19 AA;
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                                                             2093 MW;
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6, Last annotation update)
protein L18 alpha (Fragment).
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!!AA_SEQUENCE 1.0
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
CMETI-B-TRYPSIN inhibitor.
                                                                                                                                                                                                                                                                                                             "The correlation between heat-shock protein accumulation persistence and chilling tolerance in tomato fruit."; Plant Physiol. 110:531-537(1996).
SEQUENCE 16 AA; 1840 MW; 9BOD3F77BFEFECER CPPCEA.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
MEDLINE-92165927; PubMed=1791188;
Cavanaugh P.G., Nicolson G.L.;
"Lung-derived growth factor that stimulates
metastasizing tumor cells: identification as
J. Cell. Biochem. 47:261-271(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cucumis melo (Muskmelon).
                                                                                                                                                 01-WAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation updat
TRANSFERRIN-PEPTIDE 21 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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HSSP; P12071; 2ETI.
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96351184; PubMed=8742333; Sabehat A., Weiss D., Lurie S.;
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01-MAY-2000
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                                                                  SEQUENCE
                                                                                            NCBI_TaxID=10118;
                                                                                                           Mammalia; Eutheria;
                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                       Rattus sp.
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29 AA; 3196 MW; A4BCFF7AP
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Rodentia;
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                                                                                                           Craniata; Vertebrata;
Sciurognathi; Muridae;
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RX MEDLING-21085660; pubmed-11217851;
RA Arakawa T., Hara A., Fukunishi Y., Konno M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehi P., Jeruno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Sakai K., Qkido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Mynshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Havashizaki Y...
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  Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito
                                                                                    SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=EMBRYO;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
EMBL; AKO21007; BAB32275.1; ...
MGD; MGI:1926130; B330218P12Rik.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
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Mammalia; Eutheria; Rodentia;
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12
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                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; I Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                             Last annotation update)
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Fukuda S.,
samanaka I.,
Saito R.,
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RRP OCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Gurincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Lyons P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Toyo-oka K., Wang K., H., Weitz C., Whittaker C., Wilming L., Waynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Havashiraki V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q63990 PRELIMINARY; PRT; 25 AA. Q63990; Q1-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Hox3.5 homeobox homolog protein (Fragment).
                                                                Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                             DNA-binding; Homeobox; Nuclear protein.
NON_TER 1 1
NON_TER 25 25
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
STRAIN=C57BL6;
                 SEQUENCE FROM N.A
                                                  NCBI_TaxID=10090;
                                                                                                       Mus musculus (Mouse)
                                                                                                                          MSZF76
                                                                                                                                            Mszf76 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                limura T., Olda S., Takeda K., Maruoka Y., Sasaki S.; "Changes in homeobox-containing gene expression during ectopic bone formation induced by bone morphogenetic protein."; Biophys. Res. Commun. 201:980-987(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-WISTAR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:685-690(2001).
EMBL; AK019213; BAB31604.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                         Length: 25
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m; PD000010; Homeobox; 1.
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                                                                                                                                                                                                                                                                                                                                                              3111 MW;
                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                           Last sequence update)
Last annotation updat
                                                                                                                                                                                                Created)
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                                                                    Murinae; Mus
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!!AA_SEQUENCE 1.0
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O1-MAY-2000 (TrEMBLrel. 13, Created)

O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)

O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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             STRAIN=129/SVJ; TISSUE-LIVER;
MEDLINE=20102720; PubMed=10536908;
MEDLINE=20102720; PubMed=10536908;
Meditale C., Pailga K., Kreger S., Masters C.L., B
Bergsdorf C., Pailga K., Kreger S., Masters C.L., B
"Identification of cis-Elements Regulating Exon 15
Amyloid Precursor Protein Pre-mRNA.";
J. Biol. Chem. 275:2046-2056(2000).
EMBL; AF199005; AAF20194.1; -.
                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09JIIU:
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Agata Y., Matsuda E., Shimizu A.; "Rapid and efficient cloning of cDNAs encoding Krueppel-like zinc finger proteins by degenerate PCR."; Gene 213:55-64(1998).

EMBL, AB010321, BAA31377.1; ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Johnson K.J., Patel S.R., Boekelheide K.;
"Multiple cadherin superfamily members with unique expression profiles are produced in rat testis.";
Endocrinology 141:675-683(2000).
EMBL; AF177699; AAF87074.1; -.
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MEDLINE=20114371; PubMed=10650949;
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SMART; SM00355; Znf_C2H2; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
                                                                                                                                                                                                                  Amyloid protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
EMBL; AF199003; AAF20194.1; JOINED
                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                         NCBI_TaxID=10090
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                                                                                                                                                                                                                                                                                                                                                                                                             3369 MW;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation updat
Calcineurin A alpha (EC 3.1.3.16) (Fragment).
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            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                  Spermatogenic-specific proenkephalin PENK-RS.
                                                                                                                                                                                                                                                                  calcineurin A alpha gene.";
Biochem. J. 288:801-805(1992).
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Mammalia; Eutheria; Rodentia;
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NCBI_TaxID=10090;
                                       Mus musculus (Mouse)
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20 AA; 2188 MW;
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                                                                    MEDLINE-96315660; PubMed-8754834; Shago M., Giquere V.; Shago M., Giquere V.; "Isolation of a novel retinoic acid-responsive gene genomic fragments derived from CpG-tsland-enriched D Mol. Cell. Biol. 16:4337-4348(1996).
EMBL; U50384; ABB38132.1; "...
MGDJ; MGII.08048; Rrg1.
NGN_TER 32 32
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Eukaryota; Metazoa;
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EMBL; M55181; AAA40127.1;
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Kilpatrick D.L., Zinn S.A., Fitzgerald M., Higuchi H., Sabol S.L.,
Meyerhardt J.;
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ProDom; PD000010; Homeobox; 1.
DNA-binding; Homeobox; Nuclear protein.
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Mammalia; Eutheria;
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protein (Fragment).
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 2.8 kDa protein.
Mus musculus (Mouse).
Enkarrones. Tree
          Nakashima N., Miyazaki K., Ishikawa M., Yatohgo T., Ogawa H., Uchibori H., Watsumoto I., Seno N., Hayashi M.;
"Vitronectin diversity in evolution but uniformity in ligand binding and size of the core polypeptide.";
Biochim. Biophys. Acta 1120:1-10(1992).
                                                                                                                                      Cavia (guinea pigs).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae
                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                 SEQUENCE 1.0
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Submitted (FEB-2001)
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01-JUN-2001 (TrEMBLrel.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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NON_TER
                                                                                 MEDLINE=92207982; PubMed=1372829;
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Mammalia; Eutheria; Rodentia; Sciurognathi;
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                                                                                                                                                                                                                                                                                                                        Length: 27
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                                                                                                                                                                                                                                                                                              MASLPVVGSQ VPADRGYLGP RPAVQEH
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                                                                                                                                                                                                                                                                                                                                                                                BC003968; AAH03968.1;
. Biophys.
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                                                                                                                                                                                                                                                                                                                          December 22,
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                                                                                                                                                                                                                                                                                                                                                    4008F368AF868B63 CRC64;
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                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                      PRT;
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                                                    M., Yatohgo T., Ogawa
Hayashi M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mammary gland."; Blochem. Blophys. Res. Commun. 191:61-69(1993).
HMSP; P05413; 1HMT.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
SLP-14-FATTY acid-binding protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bansal M.P., Medina D.; "Expression of fatty acid-binding proteins in the developing mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                            O61461;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Cytochrome P-450b (Phenobarbital-inducible) (Fragment).
                                                                                                                                                                                                                                                                   "In vivo sucrase-isomaltase and lactase-phiorizin hydrolase turnover in the fed adult rat.";
J. Biol. Chem. 268:13609-13616(1993).
SEQUENCE 17 AA; 1947 MW; 08941FD316F9692F CRC64.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                           Dudley M.A., Hachey D.L., Quaroni A., Hutchens T.W., Nichols B.L., Rosenberger J., Perkinson J.S., Cook G., Reeds P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lactase-phlorizin hydrolase (Fragment).
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                                                  Mus musculus (Mouse).
                                                                  CYP2B13.
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93293888; PubMed=8514793;
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                                                                                                                                                                                                                 DWEDRNFIAA GPLTNDL
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!!AA_SEQUENCE 1.0
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Q66538 Length: 35 December 22, 2002 19:30
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
3. proximal protein (Fragment).
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Bluetongue virus.
Viruses; dsRNA viruses; Reoviridae; Orbivirus
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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"Characterization of a cDNA clone for mouse phenobarbital-inducible cytochrome p-450b.";
Cytochrome p-450b.";
DNA 3:129-137(1984);
                                      Virology 149:251-254(1986).
EMBL; M33062; AAA42976.1; -.
NON_TER 35 35
                                                                               KILEY M.P., Wilusz J., McCormick J.B., Keene J.D.;
"Conservation of the 3' terminal nucleotide sequences of Ebola and
Marburg virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alteration at a neutralization site in the outer coat protein, VP2."; Virology 165:23-32(1988).
EMBL: M21355; AAA42845.1; ...
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MEDLLNE=89265863; PubMed=2838961;

Gould A.R., Hyatt A.D., Eaton B.T.;

"Morphogenesis of a bluetongue virus variant with an amino acid."
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                                                                                                                                                                                       Viruses; ssRNA negative-strand viruses; Mononegavirales; Filoviridae; Ebola-like viruses.
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                                                                                                                                                                                                                  Ebola virus
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Pfam; PF00898; Orbi_VP2; 1.
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                            SEQUENCE 35 AA; 4142 MW;
                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                        NCBI_TaxID=11268;
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MGI:88599; CYP2b13.
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                                                                                                                                                                                                                                                                                                                                                                                                        19 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                         2608 MW;
                            F7778E5FC6283092 CRC64;
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Type: P Check: 8137
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1 MRKINNFLSL KFDDRNLKLK LLICNHTVDS EPHTS

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ID Q9PWC1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                084254;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and potential cyclization sequences.";
J. Mol. Biol. 198:33-41(1987).
EMBL; M35172; AAA66627.1; -.
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                                   Actinopterygii, Neopterygii; Teleostel; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                            Brachydanio rerio (Zebrafish) (Zebra danio)
Eukaryota; Metazoa; Chordata; Craniata; Veri
                                                                                                                  O9PWC1;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
p55-related MAGUK protein DLG3 (Fragment).
                                                                                                                                                                                                                                                                                                                    Stamps A.C., Campo M.S.;
"Mapping of two novel transcripts of Bovine papillomavirus type 4.";
J. Gen. Virol. 69:3033-3045(1988).
BBBL; M35264; AAA46926.1;
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Koenig C.,
                                                                                                         DLG3
                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hahn C.S., Hahn Y.S., Rice C.M., Lee E., Dalgarno L.,
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             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein (Fragment).
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Yan Y.L.,
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                                                                                                                                                                                                                                                                                  2273 MW;
Postlethwait J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
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Wendler S., Campos-Ortega J.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 AA
                                                                                Vertebrata; Euteleostomi;
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Q9PWC1 Length: 39 December 22,
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EMBL: AF124436; AAD39393.1; -.
InterPro: IPR004172; L27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopteryqii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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InterPro; IPR001356; Homeobox.
Pfam, PF00046; homeobox; 1.
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Dietrich S., Schul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-MAR-2002 (TrEMBLrel. 20, 101-MAR-2005) (Fragment).
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                                   EMBL; L09693; AAA49178.1; -.
InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                     "Homeobox genes are expressed in the retina and brain goldfish."; % \frac{\partial f}{\partial x} = \frac{\partial f}{\partial x} + \frac{
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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MEDLINE=93219357; PubMed=8096640;
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PRINTS; PR00024; HOMEOBOX
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                                                                                                                                                                                                                                                                                                                      Levine E.M., Schechter N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7957;
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                                                                                                                                                                             Natl. Acad. Sci. U.S.A. 90:2729-2733(1993).
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                                                                                                                                                                                                                     Pendleton J.W., Nagai B.K., Murtha M.T., Ruddle F.H.; "Expansion of the Hox gene family and the evolution of chordates."; Proc. Natl. Acad. Sci. U.S.A. 90:6300-6304(1993). EMBL; L14895; AAA02530.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                      Petromyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
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  LFNMYLTRER
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                                                                              ΑA;
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RLEISRGVNL TDRQVKI
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Teleostei;
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                                        2002 19:30
                                                                                 5529340A951607BD CRC64;
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Ostariophysi;
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P83009;
01-0CT-2001
01-0CT-2001
01-JUN-2002
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Petromyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Petromyzontiformes; Petromyzontidae; Petromyzon.
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Eukaryota; Metazoa; Chor
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01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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073591
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PRINTS;
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"Multiplex display polymerase chain reaction amplifies and resolves
related sequences sharing a single moderately conserved domain.";
Anal. Biochem. 256:158-168(1998).
                                                                                                                                                                                                                                                                                                                   STRAIN=WHITE LEGHORN;
MEDLINE=98141813; PubMed=9473273;
                                                                               01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Phospholemman (FXYD domain-containing ion transport
                                                                                                                                                                                                                          SEQUENCE
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NCBI_TaxID=7849;
[1]
                                  Elasmobranchii;
                                              Eukaryota;
                                                        Lamna nasus
                       Lamna
                                                                     (Fragment).
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27 AA;
                                 Metazoa; Chordata;
chii; Galeomorphii;
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Neognathae; Galliformes; Phasianidae; Phasiani
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Last annotation updat
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                                  Craniata; Vertebrata; Chondrichthyes; Galeoidea; Lamniformes; Alopiidae;
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                                                                                 regulator
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P83010
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SIMILARITY: BELONGS TO THE EXID FAMILY.

InterPro; IPR00272; ATPIGL_PLM_MATB.

PROSITE; PS01310; FXYD; PARTIAL.

Transmembrane; Phosphorylatton.
         01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                SEQUENCE
 HoxClla
                                                                                                                                                                                                                                                                                                                                     Schuurmans Stekhoven F.M.A.H., Flik G., Wendelaar Bonga S.E.; "Phospholemman in the rectal gland of sharks."; submitted (JUN-2001) to the SWISS-PROT data bank.
-!- FUNCTION: INDUCES A HYPERPOLARIZATION-ACTIVATED CHLORIDE CURRENT WHEN EXPRESSED IN XENOPUS OCCYTES. MAY HAVE A FUNCTIONAL ROLE IN MUSCLE CONTRACTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _SEQUENCE 1.0
P83010
                                                      Q90ZG3;
                                                                                                                                                              SEQUENCE
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"Phospholemman in the rectal gland of sharks.";
Submitted (JUN-2001) to the SWISS-PROT data bank.
-i- FUNCTION: INDUCES A HYDERPOLARIZATION-ACTIVATED CHLORIDE CURRENT WHEN EXPRESSED IN XENOPUS OCCYTES. MAY HAVE A FUNCTIONAL ROLE IN MUSCLE CONTRACTION.
-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. MICROSOMAL
                                                                                                                                                                                      Microsome.
                                                                                                                                                                                                    Transmembrane;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes; Triakidae;
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                                                                                                                                                                                                                    PROSITE;
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                                                                                                                                                                                                                      PTM: MAJOR PLASMA MEMBRANE SUBSTRATE FOR CAMP-DEPENDENT PROTEIN KINASE (PK-A) AND PROTEIN KINASE C (PK-C) IN SEVERAL DIFFERENT TISSUES. PHOSPHORYLATED IN RESPONSE TO INSULIN AND ADRENERGIC STIMULATION (BY SIMILARITY).

SIMILARITY: BELONGS TO THE FXYD FAMILY.

ELEPTO: IPRO00272; ATPIGL_PLM_MAT8.
                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. MICROSOMAL
                                                                                                                                    Length: 13
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(Fragment)
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Phosphorylation;
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1542 MW;
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containing ion transport
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!!AA_SEQUENCE 1.0
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01-JUN-2000 (TrEMBLrel. 13, L
01-JUN-2002 (TrEMBLrel. 21, L
Nonmuscle alpha-actinin 115 kl
Gallus gallus (Chicken).
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O9PS38;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLRel. 21, Last annotation update)
PO GLYCOPROTEIN-MYELIN major structural protein (Fri
Rana catesbelana (Bull frog).
Rana catesbelana (Bull frog).
Rana catesbelana (Bull frog).
Rana catesbelana; Chordata; Craniata; Vertebrata;
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Q9PS32
Q9PS32;
NON_TER
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SEQUENCE
                                                                                                                                                                                                                                                                                                                     myelin.
J. Mol.
                   chicken lung alpha-actinin.";
J. Biol. Chem. 267:25927-25933(1992)
                                  "A novel nonmuscle alpha-actinin.
                                                                MEDLINE=93100311;
                                                                            SEQUENCE
                                                                                                            Gallus
                                                     Imamura M.,
                                                                                               NCBI_TaxID=9031;
                                                                                                                     Archosauria;
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Kirschner D.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neotele Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyldae; Oryzinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                       "Phylogenetically
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93002191;
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EMBL; AB055740; BAB6:
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                                                     Masaki
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                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                   AA;
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                                                                                                                                                                                                                                                             December 22,
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                                                       PubMed=1334489;
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                                                                                                                                                                                                                                                                                                                                       conserved
                                                                                                                                                                                                                                                                                                                                                                      PubMed=1382532;
                                                                                                                  Neognathae;
                                                                                                                                                                                                                                                                                  2351 MW;
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                                                                                                                              Chordata;
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Teleostei; Euteleostei; Neoteleostei
                                                                                                                    Galliformes;
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mes; Phasianidae; Phasiani
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Ranidae; Rana
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update,
01-JUN-2000 (TrEMBLrel. 14, Last annotation update,
NAP-185 NEUROGLIA-associated protein (Fragment).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification and purification of a chicken brain neuroglia-
associated protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                 Q70140
Q70140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95050502; PubMed=7961672;
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9DU42;
01-MAR-2001
                                                                                                                                                                                                                              SEQUENCE 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                          Motomura K., Kusagawa S., Kato K., Nohtomi K., Iwin H.H., Tun Thwe M., Oo K.Y., Lwin S., Kyaw O., Zaw M., Nagai Y., Takebe Y "Emergence of new forms of human immunodeficiency virus type 1 intersubtype recombinants in central myanmar."; AIDS Res. Hum. Retroviruses 16:1831-1843(2000).
EMBL; AB043899; BAB19213.1; ".
EMBL; AB043899; BAB19213.1; ".
EnterPro; IPR000625; REV_protein.
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01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=11676;
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Viruses; Retroid
NCBI_TaxID=11676;
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TAT.
                                                                                                               01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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                                                 Human immunodeficiency virus type
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AA; 2404 MW; 73E0E6067F253442
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Last annotation update)
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Last sequence up
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                              Lentivirus
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                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN-26695 / ATCC 700392;

MEDLINE-97394467; PubMed-9252185;

MEDLINE-97394467; PubMed-9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,

Fleischmann R.D., Ketchum K.A., Klenk H.-G., Glodek A.,

Nelson K., Quackenbush J., Zhou L., Klirkness E.F., Peterson S.,

Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

Loftus B., Richardson D., Dodson R., Khalak M.D., Hickey E.K.,

McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,

McKenney K., FitzGerald L.M., Fugii C., Bowman C., Watthey L., Wallin E

Cotton M.D., Weidman J.M., Fugii C., Bowman C., Watthey L., Wallin E

Cotton M.D., Weidman J.M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gao F., Yue L., Craig S., Thornton C.L., Robertson D.L., McCutchan F.E., Bradac J.A., Sharp P.M., Hahn B.H.; McCutchan F.E., Bradac J.A., Sharp P.M., Hahn B.H.; "Genetic variation of HIV type 1 in four World Health Organization sponsored vaccine evaluation sites: generation of functional envelope (glycoprotein 160) clones representative of sequence subtypes A, B, C, and E. WHO Network for HIV Isolation and Characterization."; AIDS Res. Hum. Retroviruses 10:1359-1368(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUDMITTER (APR-1994) to the EMBL/GenBank/DDBJ databases. EMBL; U08794; AAB05175.1; ...
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SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05, 01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-MAR-2002 (TrEMBLrel. 20, Hypothetical protein HP0917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gao F., Morrison S.G., Robertson D.L., Thornton C.L.,
Karlsson G., Sodroski J., Morgado M., Galvao-Castro B
von Briesen H., Beddows S., Weber J., Sharp P.M., Sha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hahn B.H.;
                                                       EMBL; AE000601; AAD07968.1; -.
TIGR; HP0917; -.
Hypothetical protein; Complete
SEQUENCE 23 AA; 2717 MW; FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                             pylori.";
Nature 388:539-547(1997).
                                                                                                                                                                                                                                     "The complete genome sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=210;
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Length:
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ARDLINE-9825987; probhed-9634230;
AROCOLE S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
AROCOCK S.T., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
ARA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
ARA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
ARA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
ARA Davies R., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
ARA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
ARA Oliver S., Seeger K., Skelton S., Squares R.,
ARA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
ARA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
ARA Complete genome sequence.";
ARA Davies R., Stature 393:537-544(1998).
ARA Tuberculist; Rv35990; -.
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O06283;
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Hypothetical protein RV3599c.
RV3599C OR MTCYO7H7B.23.
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Q9KLI3;
                                                                                                                                                                                                                                                                                                                                                      STRAIN=EL TOR N16961 / SEROTYPE 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical VC0735.
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Bacteria; Firmicutes; Actinobacteria;
                                                                                                                                                                   EMBL; AE004159; AAF93900.1; -. TIGR; VC0735; -.
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                                                                                                                                Hypothetical protein; Complete proteome.
SEQUENCE 33 AA; 3661 MW; A3AD77F43D6FE40C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                        Nature 406:477-483(2000)
                                                                                                                                                                                                                                       *DNA sequence of both chromosomes
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STRAIN-EL TOR N.16961 / SEROTYPE 01;

MEDLINN=20406833; PubMed=10952301;

MEDLINN=20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Ermolaeva M.D., Vamathevan J., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Seller

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J
                                                                                                                                                                                                                                                                                                                                                                                                                             Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."

"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."

Nature 409:529-533(2001).

EMBL, AE005252; AAG55068.1; -
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical protein VCA0761.
                                                 Hypothetical protein MT3536.
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01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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Fraser C.M.;
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SEQUENCE 13 AA; 1575
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MEDLINE=21074935; PubMed=11206551;
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Bacteria; Firmicutes;
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SEQUENCE 32 AA; 3898
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MT3536.
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98 MW; E08F60B7C8C67F83 CRC64;
Actinobacteria; Actinobacteridae,
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Q9HNL3;
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
                                                                                                       MEDLINE-20504483; PubMed=11016950; Mg W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M., Mg W.V., Kennedy S.R., Baliga N.S., Thorsson V., Sbrogna J., Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J., Shukla H.D., Lasky S.R., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Welt D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Kelber K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H., Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H., Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.; "Genome sequence of Halbbacterium species NRC-1"; Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                                                                                                    Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteria;
Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR; MT3536; -.
Hypothetical protein.
SEQUENCE 35 AA; 4204 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Whole genome comparison of Mycobacterium tuberculosis clinical and Laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AE007158; AAK47876.1; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

STRAIN=CDC 1551 / OSHKOSH;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Beland D., Eisen J.A., Ermolaeva M.D., Salzberg S.L.,

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,

Belober A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome. SEQUENCE 32 AA;
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKYKLAILDE YDRADRTERG AILRRENLYS SLLTE
MVRVPVTDAG RAEMRERADR LETTAAFWRL VD
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                                 December 22, 2002 19:30 Type: P Check: 9872
                                                                        3719 MW;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                        D0F9677E650A578A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002 19:30 Type: P Check: 8356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   897851C24908FC03 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Halobacteriales;
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!!AA SEQUENCE 1.0
F1;A21630 - cytochrome P450b - mouse (fragment)
N; Contains: oxidoreductase (EC 1.-.-.)
C; Species: Mus musculus (house mouse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 11-Jun-1999
C; Accession: A21630
R;Stupans, I.; Ikeda, T.; Kessler, D.J.; Nebert, D.W.
DNA 3, 129-137, 1984
A; Title: Characterization of a cDNA clone for mouse phenobarbital-inducible
 cytochrome p-450b.
A; Reference number: A21630; MUID: 84207435; PMID: 6547088
A: Accession: A21630
A; Molecule type: mRNA
A; Residues: 1-25 <STU>
A;Cross-references: GB:K02409; NID:g192896; PIDN:AAA37510.1; PID:g553905
A; Note: the authors translated the codon CTA for residue 5 as Pro, ACC for
 residue 7 as Ser and AGT for residue 12 as Thr
C; Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C; Keywords: electron transfer; heme; monooxygenase; oxidoreductase;
 transmembrane protein
 A21630 Length: 25 December 22, 2002 19:21 Type: P Check: 4925 ..
       1 SHRLPTLDDR SKMPYTDAVI HEIQR
!!AA SEQUENCE 1.0
F1; F\overline{4}2762 - C 3.4.25.1 proteasome endopeptidase complex () subunit 13 - bovine
 (fragment)
C; Species: Bos primigenius taurus (cattle)
C;Date: 04-Mar-1993 #sequence revision 18-Nov-1994 #text change 03-Jun-2002
C; Accession: F42762
R; Dick, L.R.; Moomaw, C.R.; Pramanik, B.C.; DeMartino, G.N.; Slaughter, C.A.
Biochemistry 31, 7347-7355, 1992
A; Title: Identification and localization of a cysteinyl residue critical for
 the trypsin-like catalytic activity of the proteasome.
A; Reference number: A42762; MUID: 92378961; PMID: 1510924
A; Accession: F42762
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-20 <DIC>
A; Note: sequence extracted from NCBI backbone (NCBIP:112175)
C; Superfamily: multicatalytic endopeptidase complex chain C9
C; Keywords: hydrolase
 F42762 Length: 20 December 22, 2002 19:21 Type: P Check: 5572 ...
       1 MKGKNXVAIA ADRRFGIQAQ
 !!AA SEQUENCE 1.0
F1; S\overline{5}5729 - orotidine-5'-monophosphate decarboxylase - Aspergillus awamori
  (fragments)
C; Species: Aspergillus awamori
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-1999
C; Accession: S55729
R; Gouka, R.J.; Hessing, J.G.M.; Stam, H.; Musters, W.; van den Hondel,
 C.A.M.J.J.
Curr. Genet. 27, 536-540, 1995
A; Title: A novel strategy for the isolation of defined pyrG mutants and the
 development of a site-specific integration system for Aspergillus awamori.
 A; Reference number: S55729; MUID: 96031709; PMID: 7553938
 A; Accession: S55729
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-18;19-28 <GOU>
 C; Superfamily: orotidine-5'-phosphate decarboxylase; orotidine-5'-phosphate
 decarboxylase homology
  S55729 Length: 28 December 22, 2002 19:21 Type: P Check: 1645 ..
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1 VTVSADVTTT KELLDLADRV MGFVSTRS

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!!AA SEQUENCE 1.0
P1;B44336 - neurotoxin Tx3-2 - spider (Phoneutria nigriventer)
C; Species: Phoneutria nigriventer
C;Date: 21-Sep-1993 #sequence revision 18-Nov-1994 #text change 21-Aug-1998
C; Accession: B44336
R; Cordeiro M do, N.; de Figueiredo, S.G.; Valentim A do, C.; Diniz, C.R.; von
 Eickstedt, V.R.; Gilroy, J.; Richardson, M.
Toxicon 31, 35-42, 1993
A; Title: Purification and amino acid sequences of six Tx3 type neurotoxins from
 the venom of the Brazilian 'armed' spider Phoneutria nigriventer (Keys.).
A; Reference number: A44336; MUID: 93190315; PMID: 8446961
A; Accession: B44336
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-34 <COR>
A; Experimental source: venom
A; Note: sequence extracted from NCBI backbone (NCBIP:126773)
C; Superfamily: curtatoxin
C; Keywords: neurotoxin
 B44336 Length: 34 December 22, 2002 19:21 Type: P Check: 2946 ...
       1 ACAGLYKKCG KGASPCCEDR PCKCDLAMGN CICK
!!AA SEOUENCE 1.0
F1;B28563 - hemoglobin chain IV - earthworm (Lumbricus terrestris) (fragment)
C; Species: Lumbricus terrestris (common earthworm)
C;Date: 19-Nov-1988 #sequence revision 19-Nov-1988 #text change 04-Mar-2000
C; Accession: B28563
R; Gotoh, T.; Shishikura, F.; Snow, J.W.; Ereifej, K.I.; Vinogradov, S.N.; Walz,
Biochem. J. 241, 441-445, 1987
A; Title: Two globin strains in the giant annelid extracellular haemoglobins.
A; Reference number: A90337; MUID: 87241210; PMID: 3593201
A; Accession: B28563
A; Molecule type: protein
A; Residues: 1-22 <GOT>
C; Superfamily: globin; globin homology
C; Keywords: oxygen carrier
 B28563 Length: 22 December 22, 2002 19:21 Type: P Check: 9362 ...
       1 ADEESCCSYE DRREVRHIWD DV
!!AA SEQUENCE 1.0
F1; \overline{S01808} - hemoglobin AII - tube worm (Lamellibrachia sp.) (fragment)
C; Species: Lamellibrachia sp.
C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text change 04-Mar-2000
C; Accession: S01808
R;Suzuki, T.; Takagi, T.; Ohta, S.
Biochem. J. 255, 541-545, 1988
A; Title: N-terminal amino acid sequence of the deep-sea tube worm haemoglobin
 remarkably resembles that of annelid haemoglobin.
A; Reference number: S01807; MUID: 89076216; PMID: 3202832
A; Accession: S01808
A; Molecule type: protein
A; Residues: 1-24 <SUZ>
C; Superfamily: globin; globin homology
C; Keywords: oxygen carrier
 S01808 Length: 24 December 22, 2002 19:21 Type: P Check: 3406 ...
       1 SSNSCTTEDR REMOLMWANV WSAO
!!AA SEQUENCE 1.0
F1;D60894 - gamma crystallin V - bullfrog (fragment)
C; Species: Rana catesbeiana (bullfrog)
C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text change 21-Nov-1997
C; Accession: D60894
R; Chiou, S.H.
J. Protein Chem. 7, 527-534, 1988
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A; Title: The protein sequence homology of gamma-crystallins among major
 vertebrate classes and their DNA sequence homology to heat-shock protein genes.
A; Reference number: A60894; MUID: 89351593; PMID: 3255376
A; Accession: D60894
A; Molecule type: protein
A; Residues: 1-20 <CHI>
C; Superfamily: beta-crystallin
C; Keywords: duplication; eye lens
 D60894 Length: 20 December 22, 2002 19:21 Type: P Check: 6311 ..
       1 GKIVFYEDRN FQGRSYECSS
!!AA SEQUENCE 1.0
F1; S04621 - gamma-crystallin II - milk shark (fragment)
C; Species: Rhizoprionodon acutus (milk shark)
C;Date: 07-Sep-1990 #sequence revision 07-Sep-1990 #text change 21-Nov-1997
C; Accession: S04621
R; Chiou, S.H.
FEBS Lett. 250, 25-29, 1989
A; Title: Characterization of gamma-crystallins from eye lenses of shark: closer
 structural similarity to mammalian than other piscine gamma-crystallins?
A; Reference number: S04621; MUID: 89290026; PMID: 2737298
A; Accession: S04621
A; Molecule type: protein
A; Residues: 1-20 <CHI>
C; Superfamily: beta-crystallin
C; Keywords: duplication
 S04621 Length: 20 December 22, 2002 19:21 Type: P Check: 5853
       1 GKITFYEDRG FQGHCYECSS
!!AA SEQUENCE 1.0
F1; A61570 - gamma-crystallin (total) - siamang (fragment)
C; Species: Hylobates syndactylus (siamang)
C;Date: 25-Oct-1994 #sequence_revision 06-Jan-1995 #text_change 21-Nov-1997
C; Accession: A61570
R; Chiou, S.H.; Chang, W.P.; Ting, L.M.; Lai, T.A.; Lin, H.K.
Curr. Eye Res. 7, 1017-1022, 1988
A; Title: Biochemical characterization of lens crystallins from three mammalian
A; Reference number: A61570; MUID: 89152306; PMID: 3229121
A; Accession: A61570
A; Molecule type: protein
A; Residues: 1-20 <CHI>
A; Note: 8-Glu, 9-Gln, 10-Ala, 15-Ser, 18-Thr, and 20-Ser were also found
A; Note: this preparation appears to represent the product of several gamma
crystallin genes from one specimen
C; Superfamily: beta-crystallin
C; Keywords: duplication; eye lens
 A61570 Length: 20 December 22, 2002 19:21 Type: P Check: 6107 ..
       1 GKITFYEDRG FQGRHYECTT
!!AA SEQUENCE 1.0
F1; B61570 - gamma-crystallin (total) - Formosa sika deer (fragment)
C; Species: Cervus nippon taiouanus (Formosa sika deer)
C;Date: 25-Oct-1994 #sequence revision 06-Jan-1995 #text_change 21-Nov-1997
C; Accession: B61570
R; Chiou, S.H.; Chang, W.P.; Ting, L.M.; Lai, T.A.; Lin, H.K.
Curr. Eye Res. 7, 1017-1022, 1988
A; Title: Biochemical characterization of lens crystallins from three mammalian
 species.
A; Reference number: A61570; MUID: 89152306; PMID: 3229121
A; Accession: B61570
A; Molecule type: protein
A; Residues: 1-20 <CHI>
A; Note: 6-Phe, 14-His, and 15-Cys were also found
A; Note: this preparation appears to represent the product of several gamma
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crystallin genes from one specimen
C; Superfamily: beta-crystallin
C; Keywords: duplication; eye lens
 B61570 Length: 20 December 22, 2002 19:21 Type: P Check: 6068 ...
       1 GKITFYEDRG FQGRHYECSS
!!AA SEQUENCE 1.0
F1;A60502 - myonexin - northern leopard frog (fragment)
C; Species: Rana pipiens (northern leopard frog)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Jul-1999
C; Accession: A60502; A33087
R; Tidball, J.G.
Dev. Biol. 142, 103-114, 1990
A; Title: Myonexin: an 80-kDa glycoprotein that binds fibronectin and is located
 at embryonic myotendinous junctions.
A; Reference number: A60502; MUID: 91032554; PMID: 2146177
A; Accession: A60502
A; Molecule type: protein
A; Residues: 1-25 <TID>
C; Comment: This protein resembles calsequestrin in sequence but differs in
 distribution and physical properties.
C; Superfamily: calsequestrin
C; Keywords: fibronectin binding; glycoprotein; skeletal muscle
 A60502 Length: 25 December 22, 2002 19:21 Type: P Check: 4514 ..
       1 EDGFDFPEYD GEDRVIFISL KNYKA
!!AA SEQUENCE 1.0
F1; E33208 - calreticulin, uterine - rabbit (fragment)
C; Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 01-Mar-1996
C; Accession: E33208; F33208
R; Milner, R.E.; Baksh, S.; Shemanko, C.; Carpenter, M.R.; Smillie, L.; Vance,
 J.E.; Opas, M.; Michalak, M.
J. Biol. Chem. 266, 7155-7165, 1991
A; Title: Calreticulin, and not calsequestrin, is the major calcium binding
protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic reticulum.
A; Reference number: A33208; MUID: 91201375; PMID: 2016321
A; Accession: E33208
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-29 <MIL>
A; Note: uterine form
A; Accession: F33208
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-20 <MI2>
A; Note: hepatic form
C; Superfamily: calreticulin
 E33208 Length: 29 December 22, 2002 19:21 Type: P Check: 2821 ..
       1 EPVVYFKEQF LDGDGWTDRW IESKHKSDF
!!AA SEQUENCE 1.0
F1;C33208 - calreticulin, slow twitch skeletal muscle - rabbit (fragment)
C; Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Jul-1991 #sequence revision 31-Jul-1991 #text change 07-Feb-1997
C; Accession: C33208
R; Milner, R.E.; Baksh, S.; Shemanko, C.; Carpenter, M.R.; Smillie, L.; Vance,
 J.E.; Opas, M.; Michalak, M.
J. Biol. Chem. 266, 7155-7165, 1991
A; Title: Calreticulin, and not calsequestrin, is the major calcium binding
 protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic reticulum.
A; Reference number: A33208; MUID: 91201375; PMID: 2016321
A; Accession: C33208
A; Status: preliminary
A; Molecule type: mRNA
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A; Residues: 1-29 <MIL> C; Superfamily: calreticulin C; Keywords: skeletal muscle C33208 Length: 29 December 22, 2002 19:21 Type: P Check: 2871 ... 1 EPVVYFQFQF LDGDGWTDRW IESKHKSDF !!AA SEQUENCE 1.0 F1; A33434 - calcium-binding protein - dog (fragment) C; Species: Canis lupus familiaris (dog) C; Date: 21-Feb-1990 #sequence\_revision 21-Feb-1990 #text change 16-Feb-1997 C; Accession: A33434 R; Collins, J.H.; Xi, Z.; Alderson-Lang, B.H.; Treves, S.; Volpe, P. Biochem. Biophys. Res. Commun. 164, 575-579, 1989 A; Title: Sequence homology of a canine brain calcium-binding protein with calregulin and the human Ro/SS-A antigen. A; Reference number: A33434; MUID: 90026437; PMID: 2803321 A; Accession: A33434 A; Status: preliminary A; Molecule type: protein A; Residues: 1-24 <COL> C; Superfamily: calreticulin C; Keywords: calcium binding A33434 Length: 24 December 22, 2002 19:21 Type: P Check: 2817 .. 1 EPAIYFKEQF LDGDGXTDRX IESK !!AA SEQUENCE 1.0 F1;B41481 - virulence-associated protein (virA 5' region) - Salmonella typhimurium (fragment) C; Species: Salmonella typhimurium C; Date: 10-Apr-1992 #sequence revision 10-Apr-1992 #text\_change 20-Aug-1999 C; Accession: B41481 R; Gulig, P.A.; Chiodo, V.A. Infect. Immun. 58, 2651-2658, 1990 A; Title: Genetic and DNA sequence analysis of the Salmonella typhimurium virulence plasmid gene encoding the 28,000-molecular-weight protein. A; Reference number: A41481; MUID: 90316693; PMID: 2164511 A; Accession: B41481 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-36 <GUL> A;Cross-references: GB:M64295; GB:M33927; NID:g154440; PIDN:AAA27272.1; PID:g154441 C; Superfamily: virulence-associated protein spvB C; Keywords: DNA binding; transcription regulation B41481 Length: 36 December 22, 2002 19:21 Type: P Check: 1642 ... 1 GSQDFASQLS KLRLSDDRTA DTNRIKRIIN MRVLNS !!AA SEQUENCE 1.0  $F1; \overline{S07394}$  - DNA-invertase - phage D108 (fragment) C; Species: phage D108 A; Note: host Escherichia coli C;Date: 07-Sep-1990 #sequence revision 07-Sep-1990 #text\_change 20-Jun-2000 C; Accession: S07394 R; Szatmari, G.B.; Lapointe, M.; DuBow, M.S. Nucleic Acids Res. 15, 6691-6704, 1987 A; Title: The right end of transposable bacteriophage D108 contains a 520 base pair protein-encoding sequence not present in bacteriophage Mu. A; Reference number: S07394; MUID: 87316928; PMID: 2957646 A; Accession: S07394 A; Molecule type: DNA A; Residues: 1-22 <SZA> A; Cross-references: EMBL: X05926; NID: g14918; PIDN: CAA29365.1; PID: g1364174 C; Genetics:

A; Gene: gin C; Superfamily: transposase repressor

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C; Keywords: DNA binding; DNA integration; DNA recombination
S07394 Length: 22 December 22, 2002 19:21 Type: P Check: 9004 ..
       1 YKKHPAKRTH IENDDRINQI DR
!!AA SEQUENCE 1.0
F1;S\overline{3}5552 - vesicle-associated membrane protein 1 - mouse (fragment)
C; Species: Mus musculus (house mouse)
C;Date: 10-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 17-Mar-1999
C; Accession: S35552
R; Patarnello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.
Nature 364, 581-582, 1993
A; Title: Neurotransmission and secretion.
A; Reference number: S35552; MUID: 93354436; PMID: 8350916
A; Accession: S35552
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-32 < PAT>
C; Superfamily: synaptobrevin
S35552 Length: 32 December 22, 2002 19:21 Type: P Check: 9008 ...
       1 ERDQKLSELD DRADALQAGA SQFESSAAKL KR
!!AA SEQUENCE 1.0
F1; S\overline{3}5553 - vesicle-associated membrane protein 1 - chicken (fragment)
C; Species: Gallus gallus (chicken)
C; Date: 20-May-1994 #sequence revision 13-Mar-1997 #text change 17-Mar-1999
C; Accession: S35553
R; Patarnello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.
Nature 364, 581-582, 1993
A; Title: Neurotransmission and secretion.
A; Reference number: S35552; MUID: 93354436; PMID: 8350916
A; Accession: S35553
A; Molecule type: DNA
A; Residues: 1-32 < PAT>
C; Superfamily: synaptobrevin
 $35553 Length: 32 December 22, 2002 19:21 Type: P Check: 9118 ...
       1 ERDQKLSELD DRADALQAGA SVFESSAAKL KR
!!AA SEQUENCE 1.0
F1;S35555 - vesicle-associated membrane protein 2 - chicken (fragment)
C; Species: Gallus gallus (chicken)
C;Date: 10-Dec-1993 #sequence revision 26-Jul-1996 #text change 17-Mar-1999
C; Accession: S35555
R; Patarnello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.
Nature 364, 581-582, 1993
A; Title: Neurotransmission and secretion.
A; Reference number: S35552; MUID: 93354436; PMID: 8350916
A; Accession: S35555
A; Molecule type: DNA
A; Residues: 1-32 < PAT>
C; Superfamily: synaptobrevin
C; Keywords: membrane trafficking; transmembrane protein
 S35555 Length: 32 December 22, 2002 19:21 Type: P Check: 9033 ...
       1 ERDOKLSELD DRADALOAGA SOFETSAAKL KR
!!AA SEQUENCE 1.0
F1;S\overline{3}5554 - vesicle-associated membrane protein 2 - mouse (fragment)
C; Species: Mus musculus (house mouse)
C;Date: 10-Dec-1993 #sequence revision 27-Feb-1997 #text_change 17-Mar-1999
C; Accession: S35554
R; Patarnello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.
Nature 364, 581-582, 1993
A; Title: Neurotransmission and secretion.
A; Reference number: S35552; MUID: 93354436; PMID: 8350916
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A; Accession: S35554
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-32 < PAT>

C; Superfamily: synaptobrevin

S35554 Length: 32 December 22, 2002 19:21 Type: P Check: 9033 ...

## 1 ERDQKLSELD DRADALQAGA SQFETSAAKL KR

!!AA SEQUENCE 1.0  $F1; E\overline{4}4621$  - homeotic protein Hox 10 (clone 10w) - sea lamprey (fragment) C; Species: Petromyzon marinus (sea lamprey) C;Date: 07-Oct-1994 #sequence revision 07-Oct-1994 #text change 15-Oct-1999 C; Accession: E44621 R; Pendleton, J.W.; Nagai, B.K.; Murtha, M.T.; Ruddle, F.H. Proc. Natl. Acad. Sci. U.S.A. 90, 6300-6304, 1993 A; Title: Expansion of the Hox gene family and the evolution of chordates. A; Reference number: A44616; MUID: 93317669; PMID: 8101001 A; Accession: E44621 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-27 < PEN> A; Cross-references: GB:L14895; NID:q290813; PIDN: AAA02530.1; PID:q290814 C; Superfamily: unassigned homeobox proteins; homeobox homology C; Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation

E44621 Length: 27 December 22, 2002 19:21 Type: P Check: 9552 ...

## 1 LFNMYLTRER RLEISRGVNL TDRQVKI

!!AA SEQUENCE 1.0  $F1; F\overline{4}4621$  - homeotic protein Hox 10 (clone 10x) - sea lamprey (fragment) C; Species: Petromyzon marinus (sea lamprey) C; Date: 07-Oct-1994 #sequence revision 07-Oct-1994 #text change 15-Oct-1999 C; Accession: F44621 R; Pendleton, J.W.; Nagai, B.K.; Murtha, M.T.; Ruddle, F.H. Proc. Natl. Acad. Sci. U.S.A. 90, 6300-6304, 1993 A; Title: Expansion of the Hox gene family and the evolution of chordates. A; Reference number: A44616; MUID: 93317669; PMID: 8101001 A; Accession: F44621 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-27 < PEN> A;Cross-references: GB:L14900; NID:g290819; PIDN:AAA02535.1; PID:g290820 C; Superfamily: unassigned homeobox proteins; homeobox homology C; Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation F44621 Length: 27 December 22, 2002 19:21 Type: P Check: 9407 ...

## 1 LFSMYLTRER RLEISHLLSL TDRQVKI

# !!AA SEQUENCE 1.0 P1; $C\overline{8}4355$ - hypothetical protein Vng2049c [imported] - Halobacterium sp. NRC-1 C; Species: Halobacterium sp. NRC-1 C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text change 02-Feb-2001 C; Accession: C84355 R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.R.; Baliga, N.; Thorsson, V.; Sbrogna, J.; Swartzell, S.; Weir, D.; Hall, J.; Dahl, T.A.; Welti, R.; Goo, Y.A.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablonski, P.E.; Krebs, M.P.; Angevine, C.M.; Dale, H.; Isenbarger, T.A.; Peck, R.F.; Pohlschrod, M.; Spudich, J.L.; Jung, K.H.; Alam, M.; Freitas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000 A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Liang, P.; Riley, M.; Hood, L.; DasSarma, S. A; Title: Genome sequence of Halobacterium species NRC-1. A; Reference number: A84160; MUID: 20504483; PMID: 11016950 A; Accession: C84355 A; Status: preliminary A; Molecule type: DNA

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A; Residues: 1-32 <STO>
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A;Cross-references: GB:AE004437; NID:g10581474; PIDN:AAG20207.1; GSPDB:GN00138

C; Genetics:

A; Gene: VNG2049C

C84355 Length: 32 December 22, 2002 19:21 Type: P Check: 9872 ..

#### 1 MVRVPVTDAG RAEMRERADR LETTAAFWRL VD

!!AA SEQUENCE 1.0

P1;E64634 - hypothetical protein HP0917 - Helicobacter pylori (strain 26695)

C; Species: Helicobacter pylori

C;Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 08-Oct-1999

C; Accession: E64634

R; Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk, H.P.; Gill, S.; Dougherty, B.A.;

Nelson, K.; Quackenbush, J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, K.; Fitzegerald, L.M.; Lee, N.; Adams, M.D.; Hickey, E.K.; Berg, D.E.; Gocayne,

J.D.; Utterback, T.R.; Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.

Nature 388, 539-547, 1997

A; Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.M.; Venter, J.C.

A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A; Reference number: A64520; MUID: 97394467; PMID: 9252185

A; Accession: E64634

A; Status: preliminary; nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA

A; Residues: 1-23 < TOM>

A;Cross-references: GB:AE000601; GB:AE000511; NID:g2314051; PIDN:AAD07968.1; PID:g2314059; TIGR:HP0917

E64634 Length: 23 December 22, 2002 19:21 Type: P Check: 575 ..

## 1 MSPLTPLRNP LTQEDRFFQE IIA

!!AA SEQUENCE 1.0

F1; PHO858 - MauD protein - Paracoccus denitrificans (fragment)

C; Species: Paracoccus denitrificans

C;Date: 17-Aug-1992 #sequence\_revision 17-Aug-1992 #text\_change 08-Oct-1999

C; Accession: PH0858

R; Chistoserdov, A.Y.; Boyd, J.; Mathews, F.S.; Lidstrom, M.E.

Biochem. Biophys. Res. Commun. 184, 1181-1189, 1992

A; Title: The genetic organization of the mau gene cluster of the facultative autotroph Paracoccus denitrificans.

A; Reference number: PH0856; MUID: 92272706; PMID: 1590782

A;Accession: PH0858 A;Molecule type: DNA A;Residues: 1-23 <CHI>

A;Cross-references: GB:M90098; NID:g150580; PIDN:AAA25577.1; PID:g150581

C; Genetics: A; Gene: mauD

PH0858 Length: 23 December 22, 2002 19:21 Type: P Check: 807 ..

## 1 LEADRTGFAS LQQYMASRKK QAA

!!AA SEQUENCE 1.0

F1;  $\overline{A6}$ 1412 - methane monooxygenase (EC 1.14.13.25) protein Y - Methylococcus capsulatus (fragment)

N; Alternate names: methane hydroxylase protein Y

C; Species: Methylococcus capsulatus

C; Date: 09-Sep-1994 #sequence revision 09-Sep-1994 #text change 09-Sep-1994

C; Accession: A61412

R; Rosenzweig, A.C.; Lippard, S.J.

Acc. Chem. Res. 27, 229-236, 1994

A; Title: Determining the structure of a hydroxylase enzyme that catalyzes the conversion of methane to methanol in methanotrophic bacteria.

A; Reference number: A61412

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A; Accession: A61412
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-27 < ROS>
C; Keywords: oxidoreductase
 A61412 Length: 27 December 22, 2002 19:21 Type: P Check: 8072 ..
       1 WIEDYASRID FKADRDQIVK AVLAGLK
!!AA SEQUENCE 1.0
P1;A82288 - hypothetical protein VC0735 [imported] - Vibrio cholerae (strain
 N16961 serogroup O1)
C; Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence revision 20-Aug-2000 #text change 02-Feb-2001
C; Accession: A82288
R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.;
 Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Umayam, L.A.; Gill,
 S.R.; Nelson, K.E.; Read, T.D.; Tettelin, H.; Richardson, D.; Ermolaeva, M.D.;
 Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.; McDonald, L.;
 Utterback, T.; Fleishmann, R.D.; Nierman, W.C.; White, O.; Salzberg, S.L.;
 Smith, H.O.; Colwell, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio
 cholerae.
A; Reference number: A82035; MUID: 20406833; PMID: 10952301
A; Accession: A82288
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-33 <HEI>
A; Cross-references: GB: AE004159; GB: AE003852; NID: g9655167; PIDN: AAF93900.1;
 GSPDB:GN00126; TIGR:VC0735
A; Experimental source: serogroup O1; strain N16961; biotype El Tor
C; Genetics:
A; Gene: VC0735
A; Map position: 1
 A82288 Length: 33 December 22, 2002 19:21 Type: P Check: 3787 ..
        1 MPVGSSIPCS ISTALADRKV VSRYWCFFTL LVL
!!AA SEQUENCE 1.0
P1;B82421 - hypothetical protein VCA0761 [imported] - Vibrio cholerae (strain
 N16961 serogroup O1)
C; Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C; Accession: B82421
R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.;
 Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Umayam, L.A.; Gill, S.R.; Nelson, K.E.; Read, T.D.; Tettelin, H.; Richardson, D.; Ermolaeva, M.D.;
 Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.; McDonald, L.;
 Utterback, T.; Fleishmann, R.D.; Nierman, W.C.; White, O.; Salzberg, S.L.;
 Smith, H.O.; Colwell, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio
  cholerae.
A; Reference number: A82035; MUID: 20406833; PMID: 10952301
A; Accession: B82421
A; Status: preliminary
A; Molecule type: DNA
 A; Residues: 1-32 <HEI>
 A;Cross-references: GB:AE004404; GB:AE003853; NID:g9658174; PIDN:AAF96659.1;
  GSPDB:GN00127; TIGR:VCA0761
 A; Experimental source: serogroup O1; strain N16961; biotype El Tor
 C; Genetics:
 A; Gene: VCA0761
 A; Map position: 2
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1 MPDRLLRFSA ICSTDRRKQT NLFSSDLKQQ WR

B82421 Length: 32 December 22, 2002 19:21 Type: P Check: 1300 ..

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!!AA SEQUENCE 1.0
F1;B39089 - hydrogenase (EC 1.18.99.1) 34K chain - Thiocapsa roseopersicina
 (fragment)
C; Species: Thiocapsa roseopersicina
C;Date: 27-Nov-1991 #sequence revision 27-Nov-1991 #text_change 23-Jun-1993
C:Accession: B39089
R; Kovacs, K.L.; Tigyi, G.; Thanh, L.T.; Lakatos, S.; Kiss, Z.; Bagyinka, C. J. Biol. Chem. 266, 947-951, 1991
A; Title: Structural rearrangements in active and inactive forms of hydrogenase
 from Thiocapsa roseopersicina.
A; Reference number: A39089; MUID: 91093297; PMID: 1845998
A; Accession: B39089
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-20 <KOV>
C; Keywords: oxidoreductase
 B39089 Length: 20 December 22, 2002 19:21 Type: P Check: 6231
       1 XXEQADRPSV IGLPFQEXTG
!!AA SEQUENCE 1.0
P1;H\overline{7}0954 - hypothetical protein Rv3599c - Mycobacterium tuberculosis (strain
C; Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence revision 17-Jul-1998 #text_change 22-Oct-1999
C; Accession: H70954
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barry III, C.E.; Tekaia, F.; Badcock, K.;
 Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.;
 Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.;
 Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail,
 M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.;
 Squares, S.
Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the
 complete genome seguence.
A; Reference number: A70500; MUID: 98295987; PMID: 9634230
A; Accession: H70954
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-27 <COL>
A; Cross-references: GB: Z95557; GB: AL123456; NID: g3242276; PIDN: CAB08945.1;
 PID:e316847; PID:g2113977
A; Experimental source: strain H37Rv
C; Genetics:
A; Gene: Rv3599c
 H70954 Length: 27 December 22, 2002 19:21 Type: P Check: 8577 ..
       1 MPASSLGTGS PAADRLDATH ERRREVI
!!AA SEQUENCE 1.0
F1;S14161 - probable dTDP-4-keto-6-deoxy-hexose 3,4-isomerase (EC 5.3.99.-) -
 Saccharopolyspora erythraea (fragment)
N; Alternate names: 51K protein
C; Species: Saccharopolyspora erythraea
C; Date: 19-Mar-1997 #sequence revision 10-Oct-1997 #text change 21-Nov-1998
C; Accession: S14161
R; Caffrey, P.; Green, B.; Packman, L.C.; Rawlings, B.J.; Staunton, J.; Leadlay,
 P.F.
Eur. J. Biochem. 195, 823-830, 1991
A; Title: An acyl-carrier-protein - thioesterase domain from the
 6-deoxyerythronolide B synthase of Saccharopolyspora erythraea. High-level
 production, purification and characterisation in Escherichia coli.
A; Reference number: S14091; MUID: 91153324; PMID: 1999200
A; Accession: S14161
A; Molecule type: protein
A; Residues: 1-20 <CAF>
C; Genetics:
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A; Gene: eryCII
C; Function:
A; Description: involved in desosamine biosynthesis
C; Keywords: antibiotic biosynthesis; intramolecular oxidoreductase; isomerase
S14161 Length: 20 December 22, 2002 19:21 Type: P Check: 5957 ..
       1 MTTTDRAGLG RQLQMIRGLH
!!AA SEQUENCE 1.0
F1;\overline{86}6213 - glucose 1-dehydrogenase (EC 1.1.1.47) - Haloferax mediterranei
 (fragment)
C; Species: Haloferax mediterranei
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 30-Oct-1998
C; Accession: S66213
R;Bonete, M.J.; Pire, C.; LLorca, F.I.; Camacho, M.L.
FEBS Lett. 383, 227-229, 1996
A; Title: Glucose dehydrogenase from the halophilic Archaeon Haloferax
mediterranei: enzyme purification, characterisation and N-terminal sequence.
A; Reference number: S66213; MUID: 96198607; PMID: 8925901
A; Accession: S66213
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-17 <BON>
C; Keywords: oxidoreductase
 S66213 Length: 17 December 22, 2002 19:21 Type: P Check: 1672 ..
       1 MKAIAVKRGE DRPVVIE
!!AA SEQUENCE 1.0
P1;S23180 - carboxypeptidase - Sulfolobus solfataricus
C; Species: Sulfolobus solfataricus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C; Accession: S23180
R;Colombo, S.; D'Auria, S.; Fusi, P.; Zecca, L.; Raia, C.A.; Tortora, P.
Eur. J. Biochem. 206, 349-357, 1992
A; Title: Purification and characterization of a thermostable carboxypeptidase
 from the extreme thermophilic archaebacterium Sulfolobus solfataricus.
A; Reference number: S23180; MUID: 92283259; PMID: 1597179
A; Accession: S23180
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-31 <COL>
 S23180 Length: 31 December 22, 2002 19:21 Type: P Check: 7956 ..
       1 MDLVEKLKND VKEIEDRIIQ IRRKIXENPP L
!!AA_SEQUENCE 1.0
P1;S\overline{2}9326 - hypothetical protein 22, psbA 5'-region - Japanese black pine
 chloroplast
C; Species: chloroplast Pinus thunbergiana (Japanese black pine)
C;Date: 07-May-1993 #sequence revision 07-May-1993 #text change 18-Aug-2000
C; Accession: S29326; T07427
R;Tsudzuki, J.; Nakashima, K.; Tsudzuki, T.; Hiratsuka, J.; Shibata, M.;
 Wakasugi, T.; Sugiura, M.
Mol. Gen. Genet. 232, 206-214, 1992
A; Title: Chloroplast DNA of black pine retains a residual inverted repeat
 lacking rRNA genes: nucleotide sequences of trnQ, trnK, psbA, trnI and trnH and
 the absence of rps16.
A; Reference number: S20449; MUID: 92212283; PMID: 1557027
A; Accession: S29326
A; Status: translation not shown
A; Molecule type: DNA
A; Residues: 1-22 <TSU>
A; Cross-references: EMBL:D11467; NID:g344007; PIDN:BAA02023.1; PID:g344011
R; Wakasugi, T.; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiura, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 9794-9798, 1994
A; Title: Loss of all ndh genes as determined by sequencing the entire
 chloroplast genome of the black pine Pinus thunbergii.
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A; Reference number: Z16030; MUID: 95024047; PMID: 7937893
A; Accession: T07427
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-22 <WAK>
A;Cross-references: EMBL:D17510; NID:g529643; PIDN:BAA04307.1; PID:g1262588
C; Genetics:
A; Genome: chloroplast
C; Keywords: chloroplast
 S29326 Length: 22 December 22, 2002 19:21 Type: P Check: 9119 ...
       1 MEYLTTDRSI ECGIYLKKIE SI
!!AA SEQUENCE 1.0
F1;T10123 - probable catalase (EC 1.11.1.6) - cucumber (fragment)
C; Species: Cucumis sativus (cucumber)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C; Accession: T10123
R; Toyama, T.; Teramoto, H.; Takeba, G.; Tsuji, H.
Plant Cell Physiol. 36, 1349-1359, 1995
A; Title: Cytokinin induces a rapid decrease in the levels of mRNAs for
 catalase, 3-hydroxy-3-methylglutaryl CoA reductase, lectin and other
unidentified proteins in etiolated cotyledons of cucumber.
A; Reference number: Z16946; MUID: 96104306; PMID: 8564304
A; Accession: T10123
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-23 <TOY>
A;Cross-references: EMBL:D63385; NID:g1199475; PIDN:BAA09701.1; PID:g1199476
A; Experimental source: seedling; cotyledons
C; Keywords: oxidoreductase
 T10123 Length: 23 December 22, 2002 19:21 Type: P Check: 1444 ...
       1 NGSQADRSVG QKLAPHLNVR PSI
!!AA SEQUENCE 1.0
F1; PSO212 - 29K protein 4228 - rice (strain Nihonbare) (fragment)
C; Species: Oryza sativa (rice)
C;Date: 03-Feb-1994 #sequence revision 03-Feb-1994 #text change 11-Apr-1995
C; Accession: PS0212
R; Tsugita, A.; Miyatake, N.
submitted to JIPID, April 1993
A; Reference number: PS0208
A; Accession: PS0212
A; Molecule type: protein
A; Residues: 1-15 <TSU>
A; Experimental source: germ
C; Comment: molecular weight 29K, pI 6.1.
 PS0212 Length: 15 December 22, 2002 19:21 Type: P Check: 8963 ..
       1 SPADDRRDVG DRYAD
!!AA SEQUENCE 1.0
F1; B60698 - trichocyst protein 27 - Paramecium tetraurelia (fragment)
C; Species: Paramecium tetraurelia
C;Date: 28-Apr-1993 #sequence revision 28-Apr-1993 #text change 07-Dec-1999
C; Accession: B60698
R; Tindall, S.H.; Devito, L.D.; Nelson, D.L.
J. Cell Sci. 92, 441-447, 1989
A; Title: Biochemical characterization of the proteins of Paramecium secretory
 granules.
A; Reference number: A60698; MUID: 90078398; PMID: 2592449
A; Accession: B60698
A; Molecule type: protein
A; Residues: 1-29 <TIN>
C; Comment: This protein was purified from the extruded matrix (contents) of
 trichocysts (secretory granules).
C; Genetics:
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A; Genetic code: SGC5
C; Keywords: extracellular protein
B60698 Length: 29 December 22, 2002 19:21 Type: P Check: 2526 ..
       1 DPLDRLLSTL TDLEDRYVAE QKEDDAKNQ
!!AA SEQUENCE 1.0
F1;S19614 - globin - polychaete (Eudistylia vancouveri) (fragment)
N; Alternate names: chlorocruorin
C; Species: Eudistylia vancouveri
C; Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text change 05-Dec-1998
C; Accession: S19614
R; Qabar, A.N.; Stern, M.S.; Walz, D.A.; Chiu, J.T.; Timkovich, R.; Wall, J.S.;
Kapp, O.H.; Vinogradov, S.N.
J. Mol. Biol. 222, 1109-1129, 1991
A; Title: Hierarchy of globin complexes. The quaternary structure of the
extracellular chlorocruorin of Eudistylia vancouverii.
A; Reference number: S19532; MUID: 92106333; PMID: 1762147
A; Accession: S19614
A; Molecule type: protein
A; Residues: 1-17 < QAB>
A; Experimental source: plume
C; Complex: dodecamers, each consisting of a trimer of tetramers of globin
 chains; dodecamers are linked into bilayer structure by Ca(2+) and
heme-deficient chimeric globin chains
C; Keywords: calcium; dodecamer; heme; homotetramer; oxygen carrier
 S19614 Length: 17 December 22, 2002 19:21 Type: P Check: 1820 ..
       1 GMKXXSMEDR KTVLADW
!!AA SEQUENCE 1.0
F1; AG0741 - insulin-like growth factor-binding protein He39L - human (fragment)
C; Species: Homo sapiens (man)
C;Date: 28-Apr-1993 #sequence revision 28-Apr-1993 #text change 30-Sep-1993
C; Accession: A60741
R; Forbes, B.; Ballard, F.J.; Wallace, J.C.
J. Endocrinol. 126, 497-506, 1990
A; Title: An insulin-like growth factor-binding protein purified from medium
conditioned by a human lung fibroblast cell line (He[39]L) has a novel
 N-terminal sequence.
A; Reference number: A60741; MUID: 91011238; PMID: 1698907
A; Accession: A60741
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-25 <FOR>
 A60741 Length: 25 December 22, 2002 19:21 Type: P Check: 4352 ...
       1 LAPGPGQGVQ AGXPGGXVEE EDRGG
!!AA SEQUENCE 1.0
F1;B28457 - proteoglycan II, bone - human (tentative sequence) (fragment)
C; Species: Homo sapiens (man)
C;Date: 19-May-1989 #sequence revision 19-May-1989 #text change 31-Mar-2000
C; Accession: B28457
R; Fisher, L.W.; Hawkins, G.R.; Tuross, N.; Termine, J.D.
J. Biol. Chem. 262, 9702-9708, 1987
A; Title: Purification and partial characterization of small proteoglycans I and
 II, bone sialoproteins I and II, and osteonectin from the mineral compartment
 of developing human bone.
A; Reference number: A92656; MUID: 87250639; PMID: 3597437
A; Accession: B28457
A; Molecule type: protein
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B28457 Length: 19 December 22, 2002 19:21 Type: P Check: 4360 ...

1 DEAXGIAPEV PDDRPFEPS

A; Residues: 1-19 <FIS>

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!!AA SEQUENCE 1.0
F1; C54037 - splicing regulatory protein SWAP homolog (alternatively spliced,
 clone pFL2) - human (fragment)
C; Species: Homo sapiens (man)
C;Date: 06-Oct-1994 #sequence revision 18-Nov-1994 #text change 28-Feb-1997
C; Accession: C54037
R; Denhez, F.; Lafyatis, R.
J. Biol. Chem. 269, 16170-16179, 1994
A; Title: Conservation of regulated alternative splicing and identification of
 functional domains in vertebrate homologs to the Drosophila splicing regulator,
 suppressor-of-white-apricot.
A; Reference number: A54037; MUID: 94266805; PMID: 8206918
A; Accession: C54037
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: nucleic acid
A; Residues: 1-29 < DEN>
A; Experimental source: liver
A; Note: sequence extracted from NCBI backbone (NCBIP:149928)
 C54037 Length: 29 December 22, 2002 19:21 Type: P Check: 1565 ...
       1 POLTQEELEA KOAKOKLEDR LAAAAREKL
!!AA SEQUENCE 1.0
F1;A48845 - sterol regulatory element 1 binding protein (alternatively spliced,
 clone pCY22) - human (fragment)
C; Species: Homo sapiens (man)
C;Date: 07-Apr-1994 #sequence revision 18-Nov-1994 #text change 05-Nov-1999
C; Accession: A48845
R; Yokoyama, C.; Wang, X.; Briggs, M.R.; Admon, A.; Wu, J.; Hua, X.; Goldstein,
 J.L.; Brown, M.S.
Cell 75, 187-197, 1993
A; Title: SREBP-1, a basic-helix-loop-helix-leucine zipper protein that controls
 transcription of the low density lipoprotein receptor gene.
A; Reference number: A48845; MUID: 94006541; PMID: 8402897
A: Accession: A48845
A:Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-23 < YOK>
A; Cross-references: GB:S66168; NID:q432596; PIDN:AAB28522.1; PID:q432597
A; Experimental source: HeLa S3 cells
A; Note: sequence extracted from NCBI backbone (NCBIN:138566, NCBIN:138568,
NCBIP:138570)
A48845 Length: 23 December 22, 2002 19:21 Type: P Check: 9975 ...
       1 RGRANGTDAP RAGADRGAMD CTF
!!AA SEQUENCE 1.0
F1; S\overline{2}2228 - vitronectin - dog (fragment)
C; Species: Canis lupus familiaris (dog)
C;Date: 22-Nov-1993 #sequence revision 29-Aug-1997 #text change 29-Aug-1997
C; Accession: S22228
R; Nakashima, N.; Miyazaki, K.; Ishikawa, M.; Yatohgo, T.; Ogawa, H.; Uchibori,
H.; Matsumoto, I.; Seno, N.; Hayashi, M.
Biochim. Biophys. Acta 1120, 1-10, 1992
A: Title: Vitronectin diversity in evolution but uniformity in ligand binding
 and size of the core polypeptide.
A; Reference number: S21768; MUID: 92207982; PMID: 1372829
A; Accession: S22228
A; Molecule type: protein
A; Residues: 1-25 < NAK>
 S22228 Length: 25 December 22, 2002 19:21 Type: P Check: 4810 ..
       1 AQESXKGRVT EGFNADRKQQ QDELX
!!AA SEQUENCE 1.0
F1;A\overline{2}6393 - annexin 36K chain - pig (fragment)
C; Species: Sus scrofa domestica (domestic pig)
C;Date: 02-Jun-1988 #sequence revision 02-Jun-1988 #text change 18-Jun-1993
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C: Accession: A26393
R; Geisow, M.J.; Fritsche, U.; Hexham, J.M.; Dash, B.; Johnson, T.
Nature 320, 636-638, 1986
A; Title: A consensus amino-acid sequence repeat in Torpedo and mammalian
Ca(2)+-dependent membrane-binding proteins.
A; Reference number: A93379; MUID: 86203621; PMID: 2422556
A: Accession: A26393
A; Molecule type: protein
A; Residues: 1-16 <GEI>
   A26393 Length: 16 December 22, 2002 19:21 Type: P Check: 7 ...
       1 MLGLGTDEDR LIEIIL
!!AA SEQUENCE 1.0
P1;S68260 - hypothetical protein gadd7.1 - long-tailed hamster
C; Species: Cricetulus longicaudatus (long-tailed hamster)
C; Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C; Accession: S68260
R; Hollander, M.C.; Alamo, I.; Fornace Jr., A.J.
Nucleic Acids Res. 24, 1589-1593, 1996
A; Title: A novel DNA damage-inducible transcript, gadd7, inhibits cell growth,
but lacks a protein product.
A; Reference number: S68260; MUID: 96211359; PMID: 8649973
A; Accession: S68260
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-38 < HOL>
A; Cross-references: EMBL:L40430
 S68260 Length: 38 December 22, 2002 19:21 Type: P Check: 6375 ...
       1 MTPSFSGSSK QLQRNAQMED RGPNHPSEFI TGDNLLKT
!!AA SEQUENCE 1.0
P1;A35678 - hypothetical protein (proenkephalin 5' region) - mouse
C; Species: Mus musculus (house mouse)
C;Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 05-Nov-1999
C; Accession: A35678
R; Kilpatrick, D.L.; Zinn, S.A.; Fitzgerald, M.; Higuchi, H.; Sabol, S.L.;
Meyerhardt, J.
Mol. Cell. Biol. 10, 3717-3726, 1990
A; Title: Transcription of the rat and mouse proenkephalin genes is initiated at
distinct sites in spermatogenic and somatic cells.
A; Reference number: A35678; MUID: 90287163; PMID: 2355920
A; Accession: A35678
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-18 <KIL>
A;Cross-references: GB:M55181; NID:g201032; PIDN:AAA40127.1; PID:g201033
A35678 Length: 18 December 22, 2002 19:21 Type: P Check: 3193 ..
       1 MSSGKQDSPW EDRIPPGR
!!AA SEQUENCE 1.0
F1; PH0780 - T-cell receptor alpha chain (C11) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C; Accession: PH0780
R; Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A; Title: T cell receptor genes in a series of class I major histocompatibility
 complex-restricted cytotoxic T lymphocyte clones specific for a Plasmodium
 berghei nonapeptide: implications for T cell allelic exclusion and
 antigen-specific repertoire.
A; Reference number: PH0746; MUID: 92078846; PMID: 1836010
A; Accession: PH0780
A; Molecule type: mRNA
A; Residues: 1-15 <CAS>
A; Cross-references: EMBL:X60879
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A; Experimental source: T lymphocyte
C; Keywords: T-cell receptor
 PH0780 Length: 15 December 22, 2002 19:21 Type: P Check: 8887 ..
       1 CALSETGGAD RLTFG
!!AA SEQUENCE 1.0
F1; PHO794 - T-cell receptor alpha chain (K1 V-alpha-3.pHDS58) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence revision 17-Jul-1992 #text change 30-May-1997
C; Accession: PH0794
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A; Title: T cell receptor genes in a series of class I major histocompatibility
 complex-restricted cytotoxic T lymphocyte clones specific for a Plasmodium
berghei nonapeptide: implications for T cell allelic exclusion and
 antigen-specific repertoire.
A; Reference number: PH0746; MUID: 92078846; PMID: 1836010
A; Accession: PH0794
A; Molecule type: mRNA
A; Residues: 1-17 <CAS>
A; Cross-references: EMBL: X60899
A; Experimental source: T lymphocyte
C; Keywords: T-cell receptor
 PH0794 Length: 17 December 22, 2002 19:21 Type: P Check: 1531
       1 CAVSMNEYRG ADRLTFG
!!AA SEQUENCE 1.0
F1; PHO806 - T-cell receptor alpha chain (PE5.1.1V-alpha-8.F3.3) - mouse
 (fragment)
C; Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence revision 17-Jul-1992 #text_change 30-May-1997
C; Accession: PH0806; PH0781
R; Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A; Title: T cell receptor genes in a series of class I major histocompatibility
 complex-restricted cytotoxic T lymphocyte clones specific for a Plasmodium
 berghei nonapeptide: implications for T cell allelic exclusion and
 antigen-specific repertoire.
A; Reference number: PH0746; MUID: 92078846; PMID: 1836010
A; Accession: PH0806
A; Molecule type: mRNA
A; Residues: 1-15 <CA1>
A; Cross-references: EMBL: X60915
A; Experimental source: T lymphocyte
A; Accession: PH0781
A; Molecule type: mRNA
A: Residues: 1-15 <CA2>
A; Cross-references: EMBL:X60880
A; Experimental source: T lymphocyte
C; Keywords: T-cell receptor
 PH0806 Length: 15 December 22, 2002 19:21 Type: P Check: 8864 ..
       1 CALSDQGGAD RLTFG
!!AA SEQUENCE 1.0
F1; \overline{S03505} - T-cell receptor alpha chain J region (80) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 30-May-1997
C; Accession: S03505
R; Winoto, A.; Mjolsness, S.; Hood, L.
Nature 316, 832-836, 1985
A; Title: Genomic organization of the genes encoding mouse T-cell receptor
 alpha-chain.
A; Reference number: S03503; MUID: 85296332; PMID: 2993908
```

A; Accession: S03505 A; Molecule type: DNA

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A; Cross-references: EMBL:X02859
A: Note: this sequence was determined from the germline gene
C; Keywords: T-cell receptor
 S03505 Length: 20 December 22, 2002 19:21 Type: P Check: 6013 ..
       1 NTEGADRLTF GKGTQLIIQP
!!AA SEQUENCE 1.0
F1; PT0212 - T-cell receptor alpha chain V-J region (4-1-E.2) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text change 30-May-1997
C: Accession: PT0212
R; Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A; Title: T cell receptor V gene usage of islet beta cell-reactive T cells is
not restricted in non-obese diabetic mice.
A; Reference number: PT0209; MUID: 91217621; PMID: 1902501
A; Accession: PT0212
A; Molecule type: mRNA
A; Residues: 1-10 < NAK>
C; Keywords: T-cell receptor
 PT0212 Length: 10 December 22, 2002 19:21 Type: P Check: 3993 ...
       1 CAVAGGADRL
!!AA SEQUENCE 1.0
F1;PT0547 - T-cell receptor beta chain V-D-J region (126-1AI) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Date: 17-Jul-1992 #sequence revision 17-Jul-1992 #text change 30-May-1997
C; Accession: PT0547
R; Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta chains have few N
regions.
A; Reference number: PT0509; MUID: 91277601; PMID: 1711558
A; Accession: PT0547
A; Status: translation not shown
A; Molecule type: mRNA
A; Residues: 1-8 <FEE>
A; Experimental source: day 18 fetal thymus, strain BALB/c
C; Keywords: T-cell receptor
  PT0547 Length: 8 December 22, 2002 19:21 Type: P Check: 2627 ...
       1 ASSDADRG
!!AA SEQUENCE 1.0
F1;PT0676 - T-cell receptor beta chain V-D-J region (140-1AL) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence revision 17-Jul-1992 #text change 30-May-1997
C; Accession: PT0676
R; Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta chains have few N
 regions.
A; Reference number: PT0509; MUID: 91277601; PMID: 1711558
A; Accession: PT0676
A; Status: translation not shown
A; Molecule type: DNA
A; Residues: 1-7 <FEE>
A; Experimental source: day 18 fetal thymus, strain BALB/c
C; Keywords: T-cell receptor
  PT0676 Length: 7 December 22, 2002 19:21 Type: P Check: 2049 ..
       1 ASGEDRG
!!AA_SEQUENCE 1.0
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A; Residues: 1-20 <WIN>

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F1;PT0576 - T-cell receptor beta chain V-D-J region (141-1G) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence revision 17-Jul-1992 #text_change 30-May-1997
C; Accession: PT0576
R; Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta chains have few N
A; Reference number: PT0509; MUID: 91277601; PMID: 1711558
A; Accession: PT0576
A; Status: translation not shown
A; Molecule type: mRNA
A; Residues: 1-7 <FEE>
A; Experimental source: day 19 fetal thymus, strain BALB/c
C; Keywords: T-cell receptor
  PT0576 Length: 7 December 22, 2002 19:21 Type: P Check: 2172 ...
       1 ASSDDRT
!!AA SEQUENCE 1.0
F1; PTO366 - T-cell receptor beta chain V-J region (6R2) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text change 30-May-1997
C; Accession: PT0366
R; Lehmann, P.V.; Drexler, K.; Tary-Lehmann, M.; Falcioni, F.; Hurtenbach, U.;
Nagy, Z.A.
J. Exp. Med. 173, 333-341, 1991
A; Title: Graft-versus-host resistance induced by class II major
histocompatibility complex-specific T cell clones.
A; Reference number: PT0360; MUID: 91108330; PMID: 1824856
A; Accession: PT0366
A; Molecule type: mRNA
A; Residues: 1-28 < LEH>
C; Keywords: T-cell receptor
  PT0366 Length: 28 December 22, 2002 19:21 Type: P Check: 480 ...
       1 LYFCASSEDR NNOLRFLERG LDFSVLED
!!AA SEQUENCE 1.0
F1; A\overline{4}6592 - lactase-phlorizin hydrolase, 200K isoform - rat (fragment)
C; Species: Rattus norvegicus (Norway rat)
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 01-Nov-1996
C; Accession: A46592
R; Dudley, M.A.; Hachey, D.L.; Quaroni, A.; Hutchens, T.W.; Nichols, B.L.;
Rosenberger, J.; Perkinson, J.S.; Cook, G.; Reeds, P.J.
J. Biol. Chem. 268, 13609-13616, 1993
A; Title: In vivo sucrase-isomaltase and lactase-phlorizin hydrolase turnover in
 the fed adult rat.
A; Reference number: A46592; MUID: 93293888; PMID: 8514793
A; Accession: A46592
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-17 < DUD>
A; Note: sequence extracted from NCBI backbone (NCBIP:134559)
C; Keywords: carbohydrate digestion; intestine
 A46592 Length: 17 December 22, 2002 19:21 Type: P Check: 1363 ...
       1 DWEDRNFIAA GPLTNDL
!!AA SEQUENCE 1.0
F1; S\overline{7}8414 - ribosomal protein RL25, mitochondrial [validated] - rat (tentative
 sequence) (fragment)
C; Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1998 #sequence revision 13-Mar-1998 #text_change 21-Jul-2000
C; Accession: S78414
R; Goldschmidt-Reisin, S.; Graack, H.R.
submitted to the Protein Sequence Database, February 1998
A; Reference number: S78411
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A; Accession: S78414
A; Molecule type: protein
A; Residues: 1-26 <GOL>
A; Note: the protein is designated as mitochondrial ribosomal protein L25
C; Keywords: mitochondrion; protein biosynthesis; ribosome
 S78414 Length: 26 December 22, 2002 19:21 Type: P Check: 6086 ...
       1 ISRRXEKKNK IVYPDQLDGE DRRDAE
!!AA SEQUENCE 1.0
F1; S22227 - vitronectin - guinea pig (fragment)
C; Species: Cavia porcellus (guinea pig)
C;Date: 22-Nov-1993 #sequence revision 29-Aug-1997 #text change 29-Aug-1997
C; Accession: S22227
R; Nakashima, N.; Miyazaki, K.; Ishikawa, M.; Yatohgo, T.; Ogawa, H.; Uchibori,
H.; Matsumoto, I.; Seno, N.; Hayashi, M.
Biochim. Biophys. Acta 1120, 1-10, 1992
A; Title: Vitronectin diversity in evolution but uniformity in ligand binding
and size of the core polypeptide.
A; Reference number: S21768; MUID: 92207982; PMID: 1372829
A; Accession: S22227
A; Molecule type: protein
A; Residues: 1-25 < NAK>
 S22227 Length: 25 December 22, 2002 19:21 Type: P Check: 5585 ..
       1 XXESXKGRXT EGFNADRKXQ XXELX
!!AA SEQUENCE 1.0
F1; A\overline{5}4226 - light-harvesting protein B-830 alpha-1 chain - Chromatium
purpuratum (fragment)
C; Species: Chromatium purpuratum
C;Date: 05-Jan-1996 #sequence revision 05-Jan-1996 #text change 05-Jan-1996
C; Accession: A54226
R; Kerfeld, C.A.; Yeates, T.O.; Thornber, J.P.
Biochemistry 33, 2178-2184, 1994
A; Title: Purification and characterization of the peripheral antenna of the
purple-sulfur bacterium Chromatium purpuratum: evidence of an unusual
pigment-protein composition.
A; Reference number: A54226; MUID: 94162224; PMID: 8117674
A; Accession: A54226
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-26 < KER>
C; Keywords: antenna complex; light-harvesting polypeptide
 A54226 Length: 26 December 22, 2002 19:21 Type: P Check: 6170 ..
       1 MKVPVMMADE NAKLNNPEDD RKKFFV
!!AA SEQUENCE 1.0
F1;B\overline{5}4226 - light-harvesting protein B-830 alpha-2 chain - Chromatium
purpuratum (fragment)
C; Species: Chromatium purpuratum
C;Date: 05-Jan-1996 #sequence revision 05-Jan-1996 #text_change 05-Jan-1996
C; Accession: B54226
R; Kerfeld, C.A.; Yeates, T.O.; Thornber, J.P. Biochemistry 33, 2178-2184, 1994
A; Title: Purification and characterization of the peripheral antenna of the
 purple-sulfur bacterium Chromatium purpuratum: evidence of an unusual
 pigment-protein composition.
A; Reference number: A54226; MUID: 94162224; PMID: 8117674
A; Accession: B54226
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-23 < KER>
C; Keywords: antenna complex; light-harvesting polypeptide
  B54226 Length: 23 December 22, 2002 19:21 Type: P Check: 634 ..
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!!AA SEQUENCE 1.0
F1;T46593 - phytoene dehydrogenase [imported] - Mycobacterium marinum (fragment)
C; Species: Mycobacterium marinum
C;Date: 18-Feb-2000 #sequence revision 18-Feb-2000 #text change 21-Jul-2000
C; Accession: T46593
R; Ramakrishnan, L.; Tran, H.T.; Federspiel, N.A.; Falkow, S.
J. Bacteriol. 179, 5862-5868, 1997
A; Title: A crtB homolog essential for photochromogenicity in Mycobacterium
marinum: isolation, characterization, and gene disruption via homologous
 recombination.
A; Reference number: Z23096; MUID: 97440138; PMID: 9294446
A; Accession: T46593
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-38 < RAM>
A;Cross-references: EMBL:U92075; NID:g1928930; PIDN:AAB71427.1; PID:g1928931
A; Experimental source: strain M
C; Genetics:
A; Gene: crtI
 T46593 Length: 38 December 22, 2002 19:21 Type: P Check: 6757 ...
       1 VPGVGVPTTL ISGRLAADRI TGNTTRSIRH LDLKAQLS
!!AA SEQUENCE 1.0
P1;H85575 - hypothetical protein Z0899 [imported] - Escherichia coli (strain
O157:H7, substrain EDL933)
C; Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence revision 16-Feb-2001 #text change 14-Sep-2001
C; Accession: H85575
R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose,
 D.J.; Mayhew, G.F.; Evans, P.S.; Gregor, J.; Kirkpatrick, H.A.; Posfai, G.;
 Hackett, J.; Klink, S.; Boutin, A.; Shao, Y.; Miller, L.; Grotbeck, E.J.;
 Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, J.; Anantharaman,
 T.S.; Lin, J.; Yen, G.; Schwartz, D.C.; Welch, R.A.; Blattner, F.R.
Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A; Reference number: A85480; MUID: 21074935; PMID: 11206551
A; Accession: H85575
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-13 <STO>
A;Cross-references: GB:AE005174; NID:g12513665; PIDN:AAG55068.1; GSPDB:GN00145;
 UWGP: Z0899
A; Experimental source: strain 0157:H7, substrain EDL933
C; Genetics:
A; Gene: Z0899
 H85575 Length: 13 December 22, 2002 19:21 Type: P Check: 6940 ..
       1 MSTDRKPVML LFH
!!AA SEQUENCE 1.0
F1; PA0041 - plastoquinol-plastocyanin reductase (EC 1.10.99.1) - Arabidopsis
 thaliana (fragment)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence revision 06-Jan-1995 #text change 03-Jun-2002
C; Accession: PA0041
R; Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A; Description: Separation and characterization of Arabidopsis proteins by
 two-dimensional gel electrophoresis.
A; Reference number: PA0001
A; Accession: PA0041
A; Molecule type: protein
A; Residues: 1-15 < KAM>
A; Experimental source: leaf
C; Keywords: oxidoreductase
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PA0041 Length: 15 December 22, 2002 19:21 Type: P Check: 9117 ...

1 ASSIPADRVP DMEKR

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!!AA SEQUENCE 1.0
                                    PRT;
                                            27 AA.
     AL20 CARMA
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ID
     P81823;
AC
     30-MAY-2000 (Rel. 39, Created)
DT
     30-MAY-2000 (Rel. 39, Last sequence update)
DT
     30-MAY-2000 (Rel. 39, Last annotation update)
DT
     Carcinustatin 20.
DF.
     Carcinus maenas (Common shore crab) (Green crab).
OS
     Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
OC.
     Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
OC
     Brachyura; Eubrachyura; Portunoidea; Portunidae; Carcinus.
OC
OX
     NCBI TaxID=6759;
RN
     [1]
     SEQUENCE.
RP
     TISSUE=Cerebral ganglion, and Thoracic ganglion;
RC
     MEDLINE=98121193; PubMed=9461295;
RX
     Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA
     Thorpe A.;
RA
     "Isolation and identification of multiple neuropeptides of the
RT
     allatostatin superfamily in the shore crab Carcinus maenas.";
RT
     Eur. J. Biochem. 250:727-734(1997).
RT.
     -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC
     -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
CC
     Neuropeptide; Amidation; Multigene family.
KW
                                   AMIDATION (POTENTIAL).
FT
     MOD RES
                  27
                         27
                27 AA;
SQ
     SEQUENCE
                        3152 MW;
                                   597A6901965FE987 CRC64;
AL20 CARMA Length: 27 December 22, 2002 19:30 Type: P Check: 9046 ...
       1 GYEDEDEDRP FYALGLGKRP RTYSFGL
!!AA SEQUENCE 1.0
     AMD1 CHICK
                    STANDARD;
                                    PRT;
                                            26 AA.
ID
AC
     P81073;
     01-NOV-1997 (Rel. 35, Created)
DT
     01-NOV-1997 (Rel. 35, Last sequence update)
DT
     01-NOV-1997 (Rel. 35, Last annotation update)
DT
     AMP deaminase 1 (EC 3.5.4.6) (Myoadenylate deaminase) (AMP deaminase
DE
DE
     isoform M) (Fragment).
OS
     Gallus gallus (Chicken).
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC
OC
     Gallus.
OX
     NCBI_TaxID=9031;
RN
     [1]
RP
     SEQUENCE.
RC
     TISSUE=Breast;
RX
     MEDLINE=97269365; PubMed=9114497;
     Chilson O.P., Kelly-Chilson A.E., Siegel N.R.;
RA
RT
     "AMP-deaminases from chicken and rabbit muscle: partial primary
     sequences of homologous 17-kDa CNBr fragments: autorecognition by
RT
RT
     rabbit anti-[chicken AMPD].";
     Comp. Biochem. Physiol. 116B:371-377(1997).
RL
     -!- FUNCTION: AMP DEAMINASE PLAYS A CRITICAL ROLE IN ENERGY
CC
CC
         METABOLISM.
CC
     -! - CATALYTIC ACTIVITY: AMP + H(2)O = IMP + NH(3).
     -!- PATHWAY: PURINE NUCLEOTIDE CYCLE.
CC
CC
     -!- SUBUNIT: HOMOTETRAMER.
     -!- SIMILARITY: BELONGS TO THE ADENOSINE AND AMP DEAMINASES FAMILY.
CC
     InterPro; IPR001365; A/AMP deaminase.
DR
     PROSITE; PS00485; A DEAMINASE; PARTIAL.
DR
     Hydrolase; Nucleotide metabolism; Multigene family.
KW
FT
     NON TER
                   1
                          1
FT
     NON TER
                   26
                          26
     SEQUENCE
                26 AA;
                        3195 MW;
                                  B03E296D63BB6E75 CRC64;
SQ
AMD1_CHICK Length: 26 December 22, 2002 19:30 Type: P Check: 7006 ..
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1 MNOKHLLRFI KKSYRVDADR VVYDAK

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ID
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                    STANDARD;
                                    PRT:
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AC
     P81072;
     01-NOV-1997 (Rel. 35, Created)
DT
     01-NOV-1997 (Rel. 35, Last sequence update)
DT
     01-NOV-1997 (Rel. 35, Last annotation update)
DT
     AMP deaminase 1 (EC 3.5.4.6) (Myoadenylate deaminase) (AMP deaminase
DE
DE
     isoform M) (Fragment).
GN
     AMPD1.
OS
     Oryctolagus cuniculus (Rabbit).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
     NCBI_TaxID=9986;
OX
RN
     [1]
RP
     SEQUENCE.
     MEDLINE=97269365; PubMed=9114497;
RX
     Chilson O.P., Kelly-Chilson A.E., Siegel N.R.;
RA
     "AMP-deaminases from chicken and rabbit muscle: partial primary
RT
RT
     sequences of homologous 17-kDa CNBr fragments: autorecognition by
RT
     rabbit anti-[chicken AMPD].";
RL
     Comp. Biochem. Physiol. 116B:371-377(1997).
CC
     -!- FUNCTION: AMP DEAMINASE PLAYS 'A CRITICAL ROLE IN ENERGY
CC
         METABOLISM.
CC
     -! - CATALYTIC ACTIVITY: AMP + H(2)O = IMP + NH(3).
CC
     -!- PATHWAY: PURINE NUCLEOTIDE CYCLE.
CC
     -!- SUBUNIT: HOMOTETRAMER.
CC
     -!- TISSUE SPECIFICITY: THREE ISOFORMS ARE PRESENT IN MAMMALS: AMP
CC
         DEAMINASE 1 IS THE PREDOMINANT FORM IN SKELETAL MUSCLE; AMP
CC
         DEAMINASE 2 PREDOMINATES IN SMOOTH MUSCLE, NON-MUSCLE TISSUE,
CC
         EMBRYONIC MUSCLE AND UNDIFFERENTIATED MYOBLASTS; AMP DEAMINASE 3
CC
         IS FOUND IN ERYTHROCYTES.
CC
     -!- SIMILARITY: BELONGS TO THE ADENOSINE AND AMP DEAMINASES FAMILY.
DR
     InterPro; IPR001365; A/AMP deaminase.
DR
     PROSITE; PS00485; A DEAMINASE; PARTIAL.
     Hydrolase; Nucleotide metabolism; Multigene family.
KW
FT
     NON TER
                  1
                          1
     NON TER
                  26
                         26
FT
     SEQUENCE
                26 AA;
                        3169 MW; B022467EACBB6E75 CRC64;
SO
AMD1 RABIT Length: 26 December 22, 2002 19:30 Type: P Check: 7826 ...
       1 MNQKHLLRFI KKSYQVDADR VVYSTK
!!AA SEQUENCE 1.0
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ID
                    STANDARD;
                                   PRT;
                                            22 AA.
     Q38199;
AC
DT
     30-MAY-2000 (Rel. 39, Created)
DT
     30-MAY-2000 (Rel. 39, Last sequence update)
DΤ
     15-JUN-2002 (Rel. 41, Last annotation update)
DE
     DNA-invertase (Fragment).
GN
     GIN.
OS
     Bacteriophage D108.
OC
     Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC
     Mu-like viruses.
OX
     NCBI_TaxID=10671;
RN
     [1]
RP
     SEQUENCE FROM N.A.
RX
     MEDLINE=87316928; PubMed=2957646;
RA
     Szatmari G.B., Lapointe M., Dubow M.S.;
RT
     "The right end of transposable bacteriophage D108 contains a 520 base
RT
     pair protein-encoding sequence not present in bacteriophage Mu.";
RL
     Nucleic Acids Res. 15:6691-6703(1987).
CC
     -!- FUNCTION: THIS PROTEIN CATALYZES THE INVERSION OF A 3000-BP
CC
         SEGMENT OF PHAGE DNA. THE INVERSION RESULTS IN A MODIFICATION OF
         THE 3'END OF THE TAIL FIBER GENE AND ALTERS THE HOST SPECIFICITY.
CC
CC
     -!- SIMILARITY: BELONGS TO THE SITE-SPECIFIC RECOMBINASE RESOLVASE
CC
         FAMILY.
CC
CC
     This SWISS-PROT entry is copyright. It is produced through a collaboration
CC
     between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC
     the European Bioinformatics Institute. There are no restrictions on its
CC
     use by non-profit institutions as long as its content is in no way
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CC
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CC
      entities requires a license agreement (See http://www.isb-sib.ch/announce/
     or send an email to license@isb-sib.ch).
CC
CC
DR
      EMBL; X05926; CAA29365.1; -.
      InterPro; IPR001822; Recombinase.
DR
      PROSITE; PS00397; RECOMBINASES 1; PARTIAL.
DR
      PROSITE; PS00398; RECOMBINASES 2; PARTIAL.
DR
      DNA recombination; DNA integration; DNA-binding; DNA invertase.
KW
FT
     NON TER
                   1
                           1
                                   H-T-H MOTIF (PROBABLE).
FT
      DNA BIND
                   <1
                           5
SQ
     SEQUENCE
                 22 AA;
                         2748 MW; 097E607032767C38 CRC64;
DNIV BPD10 Length: 22 December 22, 2002 19:30 Type: P Check: 9004 ..
       1 YKKHPAKRTH IENDDRINQI DR
!!AA SEQUENCE 1.0
ID
     FIBB ANTAM
                     STANDARD;
                                    PRT;
                                            21 AA.
AC
     P14465;
     01-JAN-1990 (Rel. 13, Created)
DT
     01-FEB-1994 (Rel. 28, Last sequence update)
DT
DT
     15-JUN-2002 (Rel. 41, Last annotation update)
DΕ
     Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN
OS
     Antilocapra americana (Pronghorn).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
     Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC
OC
     Antilocapridae; Antilocapra.
OX
     NCBI TaxID=9891;
RN
     [1]
RP
     SEQUENCE.
RA
     Mross G.A., Doolittle R.F.;
RT
     "Amino acid sequence studies on artiodacty fibrinopeptides.";
RL
     Arch. Biochem. Biophys. 122:674-684(1967).
CC
     -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC
         POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC
         AGGREGATION.
CC
     -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC
         (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC
     -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC
         THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC
         CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC
         RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR
     InterPro; IPR002181; Fibrinogen C.
DR
     PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
ΚW
     Blood coagulation; Plasma; Sulfation.
FT
     PEPTIDE
                  1
                         21
                                  FIBRINOPEPTIDE B.
FT
     MOD RES
                   1
                         1
                                   PYRROLIDONE CARBOXYLIC ACID.
     MOD_RES
FT
                   6
                          6
                                  SULFATION.
     NON_TER
FT
                  21
                         21
SO
     SEQUENCE
                21 AA; 2585 MW; FCE6183BE1F31627 CRC64;
FIBB ANTAM Length: 21 December 22, 2002 19:30 Type: P Check: 7016 ...
       1 QPSYDYDEEE DDRAKLRLDA R
!!AA SEQUENCE 1.0
     FIBB BISBO
ΙD
                    STANDARD;
                                   PRT:
                                           21 AA.
     P14466;
AC
     01-JAN-1990 (Rel. 13, Created)
DT
     01-JAN-1990 (Rel. 13, Last sequence update)
     15-JUN-2002 (Rel. 41, Last annotation update)
DT
DE
     Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN
     Bison bonasus (European bison).
OS
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC
OC
     Bovidae; Bovinae; Bison.
OX
     NCBI TaxID=9902;
RN
     [1]
```

```
RA
      Blomback B., Blomback M., Grondahl N.J.;
      "Studies on fibrinopeptides from mammals.";
 RT
      Acta Chem. Scand. 19:1789-1791(1965).
 RL
      -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC
CC
          POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC
          AGGREGATION.
CC
      -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC
          (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC
      -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC
          THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC
          CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
          RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC
DR
     InterPro; IPR002181; Fibrinogen C.
DR
     PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
KW
     Blood coagulation; Plasma; Sulfation.
FT
     PEPTIDE
                   1
                          21
                                   FIBRINOPEPTIDE B.
FT
     MOD RES
                    6
                           6
                                   SULFATION.
FT
     NON TER
                   21
                          21
SQ
     SEQUENCE
                 21 AA;
                         2366 MW; 09EE75AF19E6363D CRC64;
FIBB_BISBO Length: 21 December 22, 2002 19:30 Type: P Check: 7213 ..
       1 EFPTDYDEGE DDRPKVGLGA R
!!AA SEQUENCE 1.0
ID
     FIBB BUBBU
                     STANDARD;
                                    PRT;
                                            21 AA.
AC
     P14467;
     01-JAN-1990 (Rel. 13, Created)
DT
DT
     01-FEB-1994 (Rel. 28, Last sequence update)
DΤ
     15-JUN-2002 (Rel. 41, Last annotation update)
DE
     Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN
     Bubalus bubalis (Domestic water buffalo).
OS
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
OC
     Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC
     Bovidae; Bovinae; Bubalus.
OX
     NCBI TaxID=89462;
RN
     [1]
RP
     SEQUENCE.
RA
     Mross G.A., Doolittle R.F.;
RT
     "Amino acid sequence studies on artiodacty fibrinopeptides.";
RL
     Arch. Biochem. Biophys. 122:674-684(1967).
RN
     [2]
RP
     SEQUENCE.
RC
     STRAIN=Italian breed;
RX
     MEDLINE=76040091; PubMed=1180969;
RA
     Balestrieri C., Colonna G., Irace G.;
     "Covalent structure of fibrinopeptides from buffaloes breeding in
RT
RT
     Italy.";
RL
     Biochim. Biophys. Acta 405:517-521(1975).
CC
     -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC
         POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC
         AGGREGATION.
     -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC
CC
         (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC
     -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC
         THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC
         CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC
         RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR
     InterPro; IPR002181; Fibrinogen C.
     PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
DR
KW
     Blood coagulation; Plasma; Sulfation.
FT
     PEPTIDE
                   1
                         21
                                  FIBRINOPEPTIDE B.
FT
    MOD RES
                   1
                          1
                                  PYRROLIDONE CARBOXYLIC ACID.
FT
    MOD RES
                   6
                          6
                                  SULFATION.
FT
     NON TER
                  21
                         21
SO
     SEQUENCE
                21 AA; 2379 MW; 09EE75BE4729163D CRC64;
FIBB BUBBU Length: 21 December 22, 2002 19:30 Type: P Check: 7185
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RP

SEQUENCE.

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!!AA SEQUENCE 1.0
     FIBB CEREL
                    STANDARD;
                                   PRT:
                                            21 AA.
ID
     P14468;
AC
     01-JAN-1990 (Rel. 13, Created)
DT
     01-FEB-1994 (Rel. 28, Last sequence update)
DT
     15-JUN-2002 (Rel. 41, Last annotation update)
DT
     Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
DE
GN
OS
     Cervus elaphus (Red deer), and
     Cervus elaphus nelsoni (American elk).
OS
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC
OC
     Cervidae; Cervinae; Cervus.
OX
     NCBI TaxID=9860, 9864;
RN
     [1]
     SEQUENCE.
RΡ
RC
     SPECIES=C.elaphus;
RA
     Blomback B., Blomback M., Grondahl N.J.;
RT
     "Studies on fibrinopeptides from mammals.";
RL
     Acta Chem. Scand. 19:1789-1791(1965).
RN
     [2]
     SEQUENCE.
RP
     SPECIES=C.e.nelsoni;
RC
     Mross G.A., Doolittle R.F.;
RA
RT
     "Amino acid sequence studies on artiodacty fibrinopeptides.";
RL
     Arch. Biochem. Biophys. 122:674-684(1967).
CC
     -!- FUNCTION: FIBRINGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC
         POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC
         AGGREGATION.
CC
     -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC
         (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC
     -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC
         THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC
         CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC
         RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR
     InterPro; IPR002181; Fibrinogen C.
DR
     PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
KW
     Blood coagulation; Plasma; Sulfation.
FT
     PEPTIDE
                         21
                                  FIBRINOPEPTIDE B.
                   1
FT
     MOD RES
                          1
                                  PYRROLIDONE CARBOXYLIC ACID.
                   1
     MOD_RES
FT
                   6
                          6
                                  SULFATION.
FT
     NON_TER
                  21
                         21
                        2558 MW; FCEE745D98931627 CRC64;
     SEOUENCE
                21 AA;
FIBB CEREL Length: 21 December 22, 2002 19:30 Type: P Check: 6821
       1 QHSTDYDEEE EDRAKLHLDA R
!!AA SEQUENCE 1.0
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                    STANDARD;
ID
                                    PRT:
                                            20 AA.
AC
     P14469;
     01-JAN-1990 (Rel. 13, Created)
DT
     01-JAN-1990 (Rel. 13, Last sequence update)
     15-JUN-2002 (Rel. 41, Last annotation update)
     Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN
     FGB.
OS
     Felis silvestris catus (Cat).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
     NCBI_TaxID=9685;
OX
RN
     [1]
RP
     SEQUENCE.
RA
     Blomback B., Blomback M., Grondahl N.J.;
RT
     "Studies on fibrinopeptides from mammals.";
     Acta Chem. Scand. 19:1789-1791(1965).
RL
CC
     -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
         POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC
CC
         AGGREGATION.
```

-!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS

```
(ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
     -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC
         THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC
         CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC
         RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC
     InterPro; IPR002181; Fibrinogen C.
DR
     PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
DR
     Blood coagulation; Plasma.
KW
                                   FIBRINOPEPTIDE B.
FT
     PEPTIDE
                         20
FT
     NON TER
                  20
                         20
                        2328 MW; A829E393B8F627D0 CRC64;
SO
     SEQUENCE
                20 AA;
FIBB FELCA Length: 20 December 22, 2002 19:30 Type: P Check: 5816 ...
       1 IIDYYDEGEE DRDVGVVDAR
!!AA SEQUENCE 1.0
                                            19 AA.
     FIBB LAMGL
                                    PRT;
                    STANDARD;
ID
AC
     P14473;
     01-JAN-1990 (Rel. 13, Created)
DT
     01-JAN-1990 (Rel. 13, Last sequence update)
DT
     15-JUN-2002 (Rel. 41, Last annotation update)
DT
     Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
DE
GN
     FGB.
     Lama glama (Llama),
OS
     Lama vicugna (Vicugna) (Vicugna vicugna), and
OS
     Camelus dromedarius (Dromedary) (Arabian camel).
OS
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
OC
     NCBI TaxID=9844, 9843, 9838;
OX
RN
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     SEQUENCE.
RP
RC
     SPECIES=L.glama;
     Blomback B., Blomback M., Grondahl N.J.;
RA
     "Studies on fibrinopeptides from mammals.";
RТ
RT.
     Acta Chem. Scand. 19:1789-1791(1965).
RN
     [2]
     SEQUENCE.
RP
     SPECIES=C.dromedarius;
RC
     MEDLINE=67209145; PubMed=6033721;
RX
     Doolittle R.F., Schubert D., Schwartz S.A.;
RA
     "Amino acid sequence studies on artiodactyl fibrinopeptides. I.
RТ
     Dromedary camel, mule deer, and cape buffalo.";
RT
     Arch. Biochem. Biophys. 118:456-467(1967).
RL
RN
     [3]
RP
     SEQUENCE.
     SPECIES=L.vicugna;
RC
RA
     Mross G.A., Doolittle R.F.;
     "Amino acid sequence studies on artiodacty fibrinopeptides.";
RT
     Arch. Biochem. Biophys. 122:674-684(1967).
RT.
CC
     -!- FUNCTION: FIBRINGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
         POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC
CC
         AGGREGATION.
     -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC
         (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC
CC
     -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC
         THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC
         CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC
         RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR
     InterPro; IPR002181; Fibrinogen C.
     PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
DR
     Blood coagulation; Plasma; Sulfation.
KW
                         19
                                   FIBRINOPEPTIDE B.
FT
     PEPTIDE
                   1
                   4
                           4
                                   SULFATION.
FT
     MOD RES
                  19
                         19
FT
     NON TER
                        2295 MW; E7EE6B6100568638 CRC64;
SO
     SEQUENCE
                19 AA;
FIBB LAMGL Length: 19 December 22, 2002 19:30 Type: P Check: 4317 ...
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ID
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     P14475;
AC
DT
     01-JAN-1990 (Rel. 13, Created)
     01-FEB-1994 (Rel. 28, Last sequence update)
DT
     15-JUN-2002 (Rel. 41, Last annotation update)
DT
DE
     Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN
os
     Muntiacus muntjak (Muntjak).
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
OC
     Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC
     Cervidae; Muntiacinae; Muntiacus.
OX
     NCBI_TaxID=9888;
RN
     [1]
RP
     SEOUENCE.
RA
     Mross G.A., Doolittle R.F.;
RT
     "Amino acid sequence studies on artiodacty fibrinopeptides.";
RL
     Arch. Biochem. Biophys. 122:674-684(1967).
     -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC
CC
         POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC
         AGGREGATION.
CC
     -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC
         (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC
     -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC
         THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC
         CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC
         RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
     InterPro; IPR002181; Fibrinogen C.
DR
DR
     PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
KW
     Blood coagulation; Plasma; Sulfation.
FT
     PEPTIDE
                   1
                         21
                                  FIBRINOPEPTIDE B.
FT
     MOD RES
                   1
                          1
                                  PYRROLIDONE CARBOXYLIC ACID.
FT
     MOD RES
                   6
                          6
                                  SULFATION.
                         21
FT
     NON TER
                  21
                        2514 MW; FCEE75188F0C1627 CRC64;
SQ
                21 AA;
     SEQUENCE
FIBB MUNMU Length: 21 December 22, 2002 19:30 Type: P Check: 6963 ..
       1 OHSTDYDEVE DDRAKLHLDA R
!!AA SEQUENCE 1.0
ID
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                                    PRT:
                                            21 AA.
AC
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DT
     01-JAN-1990 (Rel. 13, Created)
     01-FEB-1994 (Rel. 28, Last sequence update)
DT
     15-JUN-2002 (Rel. 41, Last annotation update)
DT
     Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
DE
GN
     FGB.
OS
     Odocoileus hemionus (Mule deer) (Black-tailed deer).
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
OC
     Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC
     Cervidae; Odocoileinae; Odocoileus.
OX
     NCBI TaxID=9872;
RN
     [1]
RΡ
     SEQUENCE.
RX
     MEDLINE=67209145; PubMed=6033721;
RA
     Doolittle R.F., Schubert D., Schwartz S.A.;
RT
     "Amino acid sequence studies on artiodactyl fibrinopeptides. I.
RT
     Dromedary camel, mule deer, and cape buffalo.";
RL
     Arch. Biochem. Biophys. 118:456-467(1967).
     -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC
CC
         POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC
         AGGREGATION.
CC
     -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC
         (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC
     -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC
         THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC
         CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC
         RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR
     InterPro; IPR002181; Fibrinogen C.
```

PROSITE; PS00514; FIBRIN\_AG\_C\_DOMAIN; PARTIAL.

DR

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Blood coagulation; Plasma; Sulfation.
KW
                   1
                         21
                                   FIBRINOPEPTIDE B.
     PEPTIDE
FΤ
                                   PYRROLIDONE CARBOXYLIC ACID.
     MOD RES
                   1
                          1
FΤ
    MOD_RES
                   6
                           6
                                   SULFATION.
FT
                  21
                          21
FT
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SQ
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                21 AA;
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     FIBB RANTA
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ID
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AC
DT
     01-JAN-1990 (Rel. 13, Created)
     01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
TC
DT
     Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
DE
GN
     Rangifer tarandus (Reindeer) (Caribou).
OS
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC
     Cervidae; Odocoileinae; Rangifer.
OC
OX
     NCBI TaxID=9870;
RN
     [1]
RP
     SEQUENCE.
RA
     Blomback B., Blomback M., Grondahl N.J.;
     "Studies on fibrinopeptides from mammals.";
RT
     Acta Chem. Scand. 19:1789-1791(1965).
RL
     -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC
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CC
CC
         AGGREGATION.
     -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC
         (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC
     -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC
         THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC
         CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC
         RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC
     InterPro; IPR002181; Fibrinogen C.
DR
     PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
DR
     Blood coagulation; Plasma; Sulfation.
KW
                                   FIBRINOPEPTIDE B.
FT
                   1
                          21
     PEPTIDE
                                   PYRROLIDONE CARBOXYLIC ACID.
     MOD RES
                   1
                           1
FT
     MOD RES
                                   SULFATION.
                           6
FT
                    6
     NON TER
                   21
                          21
FT
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SQ
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                                             21 AA.
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                                     PRT;
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AC
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DΤ
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DΤ
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     15-JUN-2002 (Rel. 41, Last annotation update)
DT
     Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
DE
GN
     FGB.
     Syncerus caffer (Cape buffalo).
OS
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC
OC
     Bovidae; Bovinae; Syncerus.
OX
     NCBI TaxID=9970;
RN
     [1]
     SEQUENCE.
RP
     MEDLINE=67209145; PubMed=6033721;
RX
     Doolittle R.F., Schubert D., Schwartz S.A.;
RA
     "Amino acid sequence studies on artiodactyl fibrinopeptides. I.
RT
     Dromedary camel, mule deer, and cape buffalo.";
RT
RL
     Arch. Biochem. Biophys. 118:456-467(1967).
```

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CC
         POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC
         AGGREGATION.
     -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC
          (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC
CC
     -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC
         THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC
         CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC
         RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR
     InterPro; IPR002181; Fibrinogen C.
DR
     PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
KW
     Blood coagulation; Plasma; Sulfation.
FT
     PEPTIDE
                    1
                          21
                                   FIBRINOPEPTIDE B.
FT
     MOD RES
                    1
                           1
                                    PYRROLIDONE CARBOXYLIC ACID.
FT
     MOD RES
                    6
                           6
                                    SULFATION.
FT
     NON TER
                   21
                          21
SQ
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!!AA SEQUENCE 1.0
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AC
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DT
     01-NOV-1997 (Rel. 35, Created)
DT
     01-NOV-1997 (Rel. 35, Last sequence update)
DT
     01-NOV-1997 (Rel. 35, Last annotation update)
DE
     Glucagon I.
OS
     Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC
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RA
     Nguyen T.M., Wright J.R. Jr., Nielsen P.F., Conlon J.M.;
RT
     "Characterization of the pancreatic hormones from the Brockmann body
RT
     of the tilapia: implications for islet xenograft studies.";
RL
     Comp. Biochem. Physiol. 111C:33-44(1995).
CC
     -!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
CC
         THE BLOOD SUGAR LEVEL.
CC
     -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS
CC
         IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
CC
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DR
DR
     InterPro; IPR000532; Glucagon.
DR
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DR
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DR
     SMART; SM00070; GLUCA; 1.
DR
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ID
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AC
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DT
     01-FEB-1994 (Rel. 28, Created)
     01-FEB-1994 (Rel. 28, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
DT
DT
DE
     Gef leader peptide.
GN
     GEFL OR B0018.
OS
     Escherichia coli.
OC
     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC
     Escherichia.
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-!- FUNCTION: FIBRINGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT

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OX
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    MEDLINE=92048481; PubMed=1943701;
RX
     Poulsen L.K., Refn A., Molin S., Andersson P.;
RA
     "The gef gene from Escherichia coli is regulated at the level of
RT
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RT
    Mol. Microbiol. 5:1639-1648(1991).
RL
RN
     SEQUENCE FROM N.A.
RP
     STRAIN=K12 / MG1655;
RC
     MEDLINE=97426617; PubMed=9278503;
RX
     Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA
     Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA
     Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA
     Mau B., Shao Y.;
RA
     "The complete genome sequence of Escherichia coli K-12.";
RТ
     Science 277:1453-1474(1997).
RL
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CC
     between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
     EMBL; AE000112; AAC73129.1; ALT TERM.
DR
     PIR; S16473; S16473.
DR
DR
     EcoGene; EG12074; gefL.
     Leader peptide; Complete proteome.
KW
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                                           14 AA.
     MY14 EISFO
ID
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     01-NOV-1995 (Rel. 32, Created)
DT
     01-NOV-1995 (Rel. 32, Last sequence update)
DT
     01-NOV-1995 (Rel. 32, Last annotation update)
DT
     Myoactive tetradecapeptide (ETP).
DE
OS
     Eisenia foetida (Common brandling worm) (Common dung-worm).
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OC
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OC
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RC
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     MEDLINE=96087879; PubMed=8532604;
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RA
RA
RT
     "A novel gut tetradecapeptide isolated from the earthworm, Eisenia
RT
     foetida.";
     Peptides 16:995-999(1995).
RL
     -!- FUNCTION: HAS A STIMULATIVE EFFECT ON THE CONTRACTION OF GUT
CC
CC
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     -!- SIMILARITY: TO INSECTS ALLATOTROPIN.
CC
KW
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                 14
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SQ
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!!AA SEQUENCE 1.0
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                                           14 AA.
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     P46980;
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
ĎΤ
DΤ
DT
     Myoactive tetradecapeptide (PTP).
DE
     Pheretima vittata (Earthworm).
OS
     Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC
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OC
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RN
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RP
RC
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     MEDLINE=96087879; PubMed=8532604;
RX
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RA
RA
     "A novel gut tetradecapeptide isolated from the earthworm, Eisenia
RT
     foetida.";
RT
     Peptides 16:995-999(1995).
RL
     -!- FUNCTION: HAS A STIMULATIVE EFFECT ON THE CONTRACTION OF GUT
CC
CC
         MUSCLES.
     -!- SIMILARITY: TO INSECTS ALLATOTROPIN.
CC
KW
     Neuropeptide; Amidation.
                                   AMIDATION.
FT
     MOD RES
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                         14
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SQ
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MY14 PHEVI Length: 14 December 22, 2002 19:30 Type: P Check: 7729 ...
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ΙD
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DT
     15-JUL-1999 (Rel. 38, Created)
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DT
     16-OCT-2001 (Rel. 40, Last annotation update)
DT
     Trichocyst matrix protein T2-A (Secretory granule protein T2-A)
DE
     (TMP 2-A) (Fragment).
DE
GN
     T2A.
     Paramecium tetraurelia.
os
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OC
OC
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OX
RN
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RP
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RC
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RX
     Madeddu L., Gautier M.-C., Vayssie L., Houari A., Sperling L.;
RA
     "A large multigene family codes for the polypeptides of the
RT
     crystalline trichocyst matrix in Paramecium.";
RТ
     Mol. Biol. Cell 6:649-659(1995).
RI.
RN
     [2]
     PARTIAL SEQUENCE.
RP
RC
     STRAIN=D4-2;
RX
     MEDLINE=95119139; PubMed=7819344;
     Madeddu L., Gautier M.-C., le Caer J.P., de Loubresse N., Sperling L.;
RΑ
     "Protein processing and morphogenesis of secretory granules in
RT
RT
     Paramecium.";
     Biochimie 76:329-335(1994).
RT.
     -!- FUNCTION: STRUCTURAL PROTEIN THAT CRYSTALLIZE INSIDE THE
CC
CC
         TRICHOCYST MATRIX.
CC
     -!- SUBCELLULAR LOCATION: TRICHOCYST. THESE ARE ARCHITECTURALLY
CC
         COMPLEX SECRETORY STORAGE GRANULES-DOCKED AT THE PLASMA MEMBRANE,
CC
         READY TO RAPIDLY RESPOND TO AN EXOCYTOTIC STIMULUS.
CC
     -!- SIMILARITY: BELONGS TO THE TMP FAMILY.
CC
     -!- DATABASE: NAME=Protein Spotlight;
CC
         NOTE=Issue 3 of October 2000;
CC
         WWW="http://www.expasy.org/spotlight/articles/sptlt003.html".
CC
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     ______
CC
     EMBL; U27509; AAA92609.1; -.
DR
     Polyprotein; Structural protein; Multigene family.
KW
FT
     NON TER
                 1
                         1
     NON TER
FT
                 23
                        23
     SEQUENCE
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                                  PRT;
                                          23 AA.
ID
AC
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DT
     15-JUL-1999 (Rel. 38, Created)
     15-JUL-1999 (Rel. 38, Last sequence update)
DT
     16-OCT-2001 (Rel. 40, Last annotation update)
DT
     Trichocyst matrix protein T2-B (Secretory granule protein T2-B)
DΕ
DE
     (TMP 2-B) (Fragment).
GN
OS
     Paramecium tetraurelia.
    Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
OC
OC
     Paramecium.
OX
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     [1]
RP
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RC
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    MEDLINE=96059477; PubMed=7579685;
RX
    Madeddu L., Gautier M.-C., Vayssie L., Houari A., Sperling L.;
RA
     "A large multigene family codes for the polypeptides of the
RТ
RТ
     crystalline trichocyst matrix in Paramecium.";
    Mol. Biol. Cell 6:649-659(1995).
RN
     [2]
     PARTIAL SEQUENCE.
RP
RC
     STRAIN=D4-2;
RX
    MEDLINE=95119139; PubMed=7819344;
RA
    Madeddu L., Gautier M.-C., le Caer J.P., de Loubresse N., Sperling L.;
RT
     "Protein processing and morphogenesis of secretory granules in
RT
     Paramecium.";
RL
     Biochimie 76:329-335(1994).
CC
     -!- FUNCTION: STRUCTURAL PROTEIN THAT CRYSTALLIZE INSIDE THE
CC
        TRICHOCYST MATRIX.
CC
    -!- SUBCELLULAR LOCATION: TRICHOCYST. THESE ARE ARCHITECTURALLY
CC
        COMPLEX SECRETORY STORAGE GRANULES-DOCKED AT THE PLASMA MEMBRANE,
CC
        READY TO RAPIDLY RESPOND TO AN EXOCYTOTIC STIMULUS.
CC
    -!- SIMILARITY: BELONGS TO THE TMP FAMILY.
CC
    -!- DATABASE: NAME=Protein Spotlight;
CC
        NOTE=Issue 3 of October 2000;
CC
        WWW="http://www.expasy.org/spotlight/articles/sptlt003.html".
CC
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    or send an email to license@isb-sib.ch).
CC
DR
    EMBL; U27510; AAA92610.1; -.
KW
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FT
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                 1
                         1
FT
    NON_TER
                 23
                        23
     SEOUENCE
               23 AA; 2706 MW; 184D4B1F2759BDB7 CRC64;
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     01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
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     01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DT
     Subtilisin/chymotrypsin inhibitor (Fragment).
DE
     Chlamydia trachomatis.
os
     Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OC
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OX
RN
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RP
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RC.
     Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
RA
     "Gene identification of Chlamydia trachomatis by random DNA
RТ
RT
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RT.
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FT
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                   1
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     NON TER
                  17
                          17
FT
                        2043 MW;
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                17 AA;
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     Q9KIL6
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     01-OCT-2000 (TrEMBLrel. 15, Created)
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     01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
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     01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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DE
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GN
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OC
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OC
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OX
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RP
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     STRAIN=M145;
RC
     Kormanec J., Sevcikova B., Homerova D.;
RA
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DR
FT
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     Q9X9U4
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AC
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DT
     01-NOV-1999 (TrEMBLrel. 12, Created)
     01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT
     01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DT
DΕ
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GN
     GLGC.
OS
     Streptomyces coelicolor.
OC
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     Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OC
OX
     NCBI_TaxID=1902;
RN
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RP
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RC
     STRAIN=A3(2);
     Bruton C.J.;
RA
     Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
RL
RN
     [2]
RP
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RC
     STRAIN=A3(2);
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MEDLINE=98062210; PubMed=9401038;
     Martin M., Schneider D., Bruton C.J., Chater K.F., Hardisson C.;
RA
     "A glgC Gene Essential Only for the First of Two Spatially Distinct
RT
     Phases of Glycogen Synthesis in Streptomyces coelicolor A3(2).";
RT
     J. Bacteriol. 179:7784-7789(1997).
RL
     EMBL; AJ243803; CAB50742.1; -.
DR
     InterPro; IPR001825; NTP transferase.
DR
     Pfam; PF00483; NTP_transferase; 1.
DR
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FT
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                         25
                25 AA;
                        2566 MW; 84B94A728A41D25C CRC64;
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SQ
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     01-NOV-1996 (TrEMBLrel. 01, Created)
     01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT
     01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DT
DE
     MxaS protein (Fragment).
GN
     MXAS.
OS
     Methylobacterium extorquens.
OC
     Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC
     Methylobacterium group; Methylobacterium.
OX
     NCBI TaxID=408;
RN
     [1]
RΡ
     SEQUENCE FROM N.A.
RC
     STRAIN=AM1;
RX
     MEDLINE=96074311; PubMed=7592474;
     Morris C.J., Kim Y.M., Perkins K.E., Lidstrom M.E.;
RA
     "Identification and nucleotide sequences of mxaA, mxaC, mxaK, mxaL,
RT
RT
     and mxaD genes from Methylobacterium extorquens AM1.";
RL
     J. Bacteriol. 177:6825-6831(1995).
DR
     EMBL; L41608; AAA85567.1; -.
FT
     NON TER
                   1
     SEOUENCE
                32 AA;
                        3700 MW;
                                  EB03BB62B3C56ED5 CRC64;
SO
 Q49137 Length: 32 December 22, 2002 19:30 Type: P Check: 9647 ...
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     01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT
DT
     01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE
     CurD protein (Fragment).
OS
     Streptomyces cyaneus (Streptomyces curacoi).
OC
     Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC
     Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX
     NCBI TaxID=1904;
RN
     SEQUENCE FROM N.A.
RP
RA
     Bergh S.T., Uhlen M.;
     "Cloning, analysis and heterologous expression of the polyketides
RТ
     synthesis genes of Streptomyces curacoi.";
RT
     Submitted (JUN-1990) to the EMBL/GenBank/DDBJ databases.
RL
DR
     EMBL; M33704; AAA26724.1; -.
FT
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                   1
                           1
                9 AA; 1027 MW;
                                 995BDDDDC4140AB1 CRC64;
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SO
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ID
     050476
                 PRELIMINARY;
                                    PRT;
                                            13 AA.
AC
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RX

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     01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT
     01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DT
DΕ
     Catalase.
GN
     KATG.
     Mycobacterium tuberculosis.
os
     Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC
     Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OC
OX
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RN
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RP
RC
     STRAIN=L10373;
     Cockerill F.R., Uhl J.R., Temesgen Z., Zhang Y., Stockman L.,
RA
RA
     Roberts G.D., Williams D.L., Kline B.C.;
     "Rapid Identification of a point mutation of the Mycobacterium
RT
     tuberculosis catalase-peroxidase (katG) gene associated with isoniazid
RT
RT
     resistance.";
RL
     Submitted (FEB-1994) to the EMBL/GenBank/DDBJ databases.
     EMBL; U06263; AAB59976.1; -.
DR
               13 AA; 1564 MW; 2F39A45EFE994777 CRC64;
SO
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 Q50476 Length: 13 December 22, 2002 19:30 Type: P Check: 7152
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     005422
                                    PRT:
                                            38 AA.
ID
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DT
DT
     01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
     01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DT
DE
     Phytoene dehydrogenase (Fragment).
GN
     CRTI.
os -
     Mycobacterium marinum.
OC
     Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
     Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OC
OX
     NCBI TaxID=1781;
RN
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RP
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RC
     STRAIN=M;
RX
     MEDLINE=97440138; PubMed=9294446;
RA
     Ramakrishnan L., Tran H.T., Federspiel N.A., Falkow S.;
RT
     "A crtB homolog essential for photochromogenicity in Mycobacterium
RT
     marinum: isolation, characterization, and gene disruption via
RT
     homologous recombination.";
RL
     J. Bacteriol. 179:5862-5868(1997).
     EMBL; U92075; AAB71427.1; -.
DR
FT
     NON TER
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                         1
     SEQUENCE
                38 AA; 3986 MW; 6E46332707CCDCAB CRC64;
SQ
 005422 Length: 38 December 22, 2002 19:30 Type: P Check: 6757 ...
       1 VPGVGVPTTL ISGRLAADRI TGNTTRSIRH LDLKAQLS
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ID
     Q93A12
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DT
     01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT
     01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE
     Putative ribitol/glucose oxidoreductase (Fragment).
GN
     SDRA2.
OS
     Thiobacillus ferrooxidans.
OC
     Bacteria; Proteobacteria; gamma subdivision; Acidithiobacillus.
OX
     NCBI TaxID=920;
RN
     [1]
RP
     SEQUENCE FROM N.A.
RC
     STRAIN=ATCC33020;
RA
     Bruscella P., Levican G., Ratouchniak J., Holmes D., Bonnefoy V.;
RT
     "A second operon encoding a bcl complex in Acidithiobacillus
RT
     ferrooxidans.";
```

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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RL
     EMBL; AJ311888; CAC44744.1; -.
DR
FT
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                22 AA; 2464 MW;
                                  3725F8E43BBA75C2 CRC64;
SO
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093A12 Length: 22 December 22, 2002 19:30 Type: P Check: 9419 ...
       1 AQNFINPDLD DRTEKDLATS TV
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ID
     Q93A08
                                   PRT;
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     Q93A08;
AC
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DT
     01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DΤ
DT
     01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DΕ
     ResB protein (Fragment).
GN
OS
     Thiobacillus ferrooxidans.
OC
     Bacteria; Proteobacteria; gamma subdivision; Acidithiobacillus.
OX
     NCBI TaxID=920;
RN
     [1]
     SEQUENCE FROM N.A.
RP
     STRAIN=ATCC33020;
RC
     Levican G., Bruscella P., Guacunano M., Inostroza C., Jedlicki E.,
RA
RA
     Bonnefoy V., Holmes D.S.;
     "Characterization of the pet and res operons of Acidithiobacillus
RT
RT
     ferrooxidans.";
RL
     Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR
     EMBL; AJ413194; CAC88360.1; -.
FT
     NON TER
                12 AA; 1405 MW; 886AB7DF1E13240A CRC64;
SQ
     SEQUENCE
 Q93A08 Length: 12 December 22, 2002 19:30 Type: P Check: 5753
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                                    PRT;
                                            19 AA.
ID
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AC
DT
     01-NOV-1996 (TrEMBLrel. 01, Created)
DT
     01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
     01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DT
DΕ
     Alpha-acceptor polypeptide M15 (Fragment).
     Escherichia coli.
OS
     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC
OC
     Escherichia.
OX
     NCBI_TaxID=562;
RN
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RP
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RC
     STRAIN=DH5 ALPHA;
RX
     MEDLINE=93083990; PubMed=1339377;
RA
     Prentki P.C.;
     "Nucleotide sequence of the classical lacZ deletion delta M15.";
RT
     Gene 122:231-232(1992).
RL
     EMBL; X58252; CAA41206.1; -.
DR
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FT
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                         19
     SEQUENCE
                19 AA; 2092 MW; 8324315E003AA053 CRC64;
SQ
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AC
DT
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DT
     01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT
     01-FEB-1997 (TrEMBLrel. 02, Last annotation update)
DE
     MKAA protein (Fragment).
os
     Salmonella typhimurium.
OG
     Plasmid pYA426.
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC
     Salmonella.
OX
     NCBI_TaxID=602;
RN
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RP
     Gulig P.A., Chiodo V.A.;
RA
     Infect. Immun. 58:2651-2658(1991).
RL
     EMBL; M64295; AAA27272.1; -.
DR
KW
     Plasmid.
FT
     NON TER
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                36 AA; 4121 MW; C3D43D1C622EBAB7 CRC64;
SO
     SEOUENCE
Q99094 Length: 36 December 22, 2002 19:30 Type: P Check: 1642
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DT
     01-OCT-2000 (TrEMBLrel. 15, Created)
DT
     01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT
     01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DΕ
     ATP7B (Fragment).
OS
     Homo sapiens (Human).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC
OX
     NCBI TaxID=9606;
RN
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RP
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RA
     Wu Z.Y., Wang N., MuRong S.X., Lin M.T., Fang L.;
     Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RL
DR
     EMBL; AF220215; AAF67661.1; -.
     InterPro; IPR001757; ATPase E1-E2.
DR
DR
     Pfam; PF00122; E1-E2 ATPase; 1.
FT
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                          1
FT
     VARIANT
                  19
                          19
                                   V -> I.
FT
                  20
     NON TER
                          20
SQ
     SEQUENCE
                20 AA;
                        2282 MW; 00268E2C1E0692E3 CRC64;
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       1 APIQQLADRF SGYFVPFIVI
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                 PRELIMINARY;
                                    PRT;
                                             40 AA.
ID
     Q15244
AC
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     01-NOV-1996 (TrEMBLrel. 01, Created)
DT
     01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT
     01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DΤ
DΕ
     Phosphoribosylpyrophosphate synthetase isoform I (Fragment).
OS
     Homo sapiens (Human).
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC
OX
     NCBI TaxID=9606;
RN
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RP
     SEQUENCE FROM N.A.
RC
     TISSUE=BLOOD;
RA
     Ishizuka T.;
RL
     Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
RN
     [2]
RP
     SEQUENCE FROM N.A.
RC
     TISSUE=BLOOD;
     MEDLINE=92223087; PubMed=1314091;
RX
     Ishizuka T., Iizasa T., Taira M., Ishijima S., Sonoda T., Shimada H., Nagatake N., Tatibana M.;
RA
RA
RT
     "Promoter regions of the human X-linked housekeeping genes PRPS1 and
     PRPS2 encoding phosphoribosylpyrophosphate synthetase subunit I and II
RT
RT
     isoforms.";
RL
     Biochim. Biophys. Acta 1130:139-148(1992).
     EMBL; D28133; BAA05675.1; -.
DR
DR
     HSSP; P14193; 1DKU.
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OC

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57C2B4011860B098 CRC64;
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SO
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       1 MPNIKIFSGS SHQDLSQKIA DRLGLELGKV VTKKFSNQET
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                                     PRT;
                                             40 AA.
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     015245;
AC
     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DT
DT
DT
     Phosphoribosylpyrophosphate synthetase isoform II (Fragment).
DE
     Homo sapiens (Human).
OS
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC
OX
     NCBI TaxID=9606;
RN
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RP
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RC
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RA
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RL
RN
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RP
RC
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     MEDLINE=92223087; PubMed=1314091;
RX
     Ishizuka T., Iizasa T., Taira M., Ishijima S., Sonoda T., Shimada H.,
RA
RA
     Nagatake N., Tatibana M.;
     "Promoter regions of the human X-linked housekeeping genes PRPS1 and
RT
     PRPS2 encoding phosphoribosylpyrophosphate synthetase subunit I and II
RT
RT
     isoforms.";
     Biochim. Biophys. Acta 1130:139-148(1992).
RL
     EMBL; D28134; BAA05676.1; -.
DR
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FT
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                         4431 MW; CEC2B31686083EFF CRC64;
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                  PRELIMINARY;
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AC
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     01-JUN-2001 (TrEMBLrel. 17, Created)
DT
     01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT
     01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DT
     L-isoaspartyl/D-aspartyl methyltransferase (Fragment).
DE
QS
     Homo sapiens (Human).
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC
OX
     NCBI TaxID=9606;
RN
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RP
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     MEDLINE=94354847; PubMed=8074695;
RX
RA
      Tsai W., Clarke S.;
      "Amino acid polymorphisms of the human L-isoaspartyl/D-aspartyl
RT
     methyltransferase involved in protein repair.";
RT
      Biochem. Biophys. Res. Commun. 203:491-497(1994).
RL
      EMBL; $73902; AAC60639.2; -.
DR
      InterPro; IPR000682; Pcmt.
DR
      Pfam; PF01135; PCMT; 1.
DR
      Methyltransferase; Transferase.
KW
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FT
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                           34
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FT
                 34 AA; 3873 MW; EEB18E55F49BF377 CRC64;
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SQ
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40

NON TER

40

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AC
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DT
     01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT
     01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DΨ
     Tropomyosin (Fragment).
DF.
     Homo sapiens (Human).
OS
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC
     NCBI TaxID=9606;
OX
RN
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RP
     SEQUENCE.
     MEDLINE=93195352; PubMed=8450225;
RX
     Das K.M., Dasgupta A., Mandal A., Geng X.;
RA
     "Autoimmunity to cytoskeletal protein tropomyosin. A clue to the
RT
     pathogenetic mechanism for ulcerative colitis.";
RT
     J. Immunol. 150:2487-2493(1993).
RL
     InterPro; IPR000533; Tropomyosin.
DR
     Pfam; PF00261; Tropomyosin; 1.
DR
                15 AA; 1802 MW; 7A0993CA5A54254C CRC64;
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SQ
 Q9UCI1 Length: 15 December 22, 2002 19:30 Type: P Check: 8961
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                                               28 AA.
ID
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АC
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DT
DT
DT
     Unknown (Protein for IMAGE: 4563468) (Fragment).
DE
     Homo sapiens (Human).
OS
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC
     NCBI TaxID=9606;
OX
RN
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     SEQUENCE FROM N.A.
RP
     TISSUE=KIDNEY;
RC
     Strausberg R.;
RA
     Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RL
      EMBL; BC011565; AAH11565.1; -.
DR
     NON TER
FΤ
                  28 AA; 2841 MW; 5799D138245D3951 CRC64;
SQ
      SEOUENCE
  Q96F68 Length: 28 December 22, 2002 19:30 Type: P Check: 588 ..
        1 VSOPGSCRHG ADRVGHVGQR AGAGVRPE
!!AA SEQUENCE 1.0
                  PRELIMINARY;
                                       PRT;
                                                26 AA.
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ΙD
AC
      Q9NBB1;
     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DT
DT
DT
      Stretchin-MLCK (Fragment).
DE
      STRN-MLCK OR CG8304 OR CG18255.
GN
      Drosophila melanogaster (Fruit fly).
OS
      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC
      Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC
      Ephydroidea; Drosophilidae; Drosophila.
OC
      NCBI TaxID=7227;
OX
RN
      [1]
RP
      SEQUENCE FROM N.A.
      Champagne M.B., Edwards K.A., Erickson H.P., Kiehart D.P.;
RA
      "Drosophila stretchin-MLCK is a Novel Member of the Titin/Myosin Light
RT
      Chain Kinase Family.";
RT
      J. Mol. Biol. 0:0-0(2000).
RL
      EMBL; AF257309; AAF90127.1; -.
DR
      FlyBase; FBgn0013988; Strn-Mlck.
DR
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FT
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                26 AA; 3004 MW; 2F2CB3A55E7FF033 CRC64;
     SEQUENCE
SQ
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       1 VVARNNFGTD RIFVTVTIKI PKKKEE
!!AA SEQUENCE 1.0
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                  PRELIMINARY;
                                     PRT;
ID
     Q9GU45
AC
     Q9GU45;
     01-MAR-2001 (TrEMBLrel. 16, Created)
DT
     01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT
     01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DT
     Homeobox protein Sycox2 (Fragment).
DE
GN
     SYCOX2.
OS
     Sycon raphanus.
     Eukaryota; Metazoa; Porifera; Calcarea; Calcaronea; Leucosoleniida;
OC
OC
     Sycettidae.
OX
     NCBI TaxID=56443;
RN
     SEQUENCE FROM N.A.
RP
     MEDLINE=20476455; PubMed=11020308;
RX
     Manuel M., Le Parco Y.;
RA
     "Homeobox Gene Diversification in the Calcareous Sponge, Sycon
RT
     raphanus.";
RT
     Mol. Phylogenet. Evol. 17:97-107(2000).
RL
     EMBL; AF197140; AAG28510.1; -.
DR
     InterPro; IPR001356; Homeobox.
DR
     Pfam; PF00046; homeobox; 1.
DR
     NON TER
FT
                    1
                           27
                   27
     NON TER
FT
                 27 AA; 2986 MW; CA58FA11B629E3B7 CRC64;
     SEQUENCE
SQ
 Q9GU45 Length: 27 December 22, 2002 19:30 Type: P Check: 9325 ..
       1 KTSKYLAPTT RQALAARLGL TDRQVKV
!!AA_SEQUENCE 1.0
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ID
AC
     Q9GU44;
     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DT
DT
DT
     Homeobox protein Sycox3 (Fragment).
DE
GN
     SYCOX3.
OS
     Sycon raphanus.
     Eukaryota; Metazoa; Porifera; Calcarea; Calcaronea; Leucosoleniida;
OC
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OC
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     NCBI TaxID=56443;
RN
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RP
     MEDLINE=20476455; PubMed=11020308;
RX
     Manuel M., Le Parco Y.;
RA
      "Homeobox Gene Diversification in the Calcareous Sponge, Sycon
RT
      raphanus.";
RT
     Mol. Phylogenet. Evol. 17:97-107(2000).
RL
      EMBL; AF197141; AAG28511.1; -.
DR
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DR
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DR
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DE
     Calmodulin (Fragment).
GN
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OS
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OC
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OC
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OX
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RP
RA
     Wilding C.S., Grahame J., Mill P.J.;
     "Molecular characterisation of calmodulin intron variation in
RT
RT
     Littorina (Gastropoda: Prosobranchia) species.";
     Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DT
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DT
DE
     PmHbox1 (Fragment).
OS
     Polyandrocarpa misakiensis.
     Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC
OC
     Stolidobranchia; Styelidae; Polyandrocarpa.
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OX
RN
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RP
RC
     STRAIN=USHIMADO;
     Fujiwara S., Kawamura K.;
RA
RT
     "Cloning of homeobox-containing genes from the budding ascidian
RT
     Polyandrocarpa misakiensis.";
RL
     Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
DR
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     01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT
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DΤ
DE
     Ovx1 ortholog homeobox (Fragment).
     CTS-OVX1.
GN
     Ctenodrilus serratus.
OS
OC
     Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
OC
     Terebellida; Ctenodrilidae; Ctenodrilus.
OX
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RN
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     MEDLINE=94356262; PubMed=7915607;
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RA
     Dick M.H., Buss L.W.;
     "A PCR-based survey of homeobox genes in Ctenodrilus serratus
RT
RT
      (Annelida: Polychaeta).";
     Mol. Phylogenet. Evol. 3:146-158(1994).
RL
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RN
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RP
     Dick M.H., Buss L.W.;
RA
     Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
RL
     EMBL; U26634; AAC46856.1; -.
DR
     DNA-binding; Homeobox; Nuclear protein.
KW
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
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DT
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DТ
     Anthox1.Ms (Fragment).
DE
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GN
     Metridium senile (Brown sea anemone) (Frilled sea anemone).
OS
     Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
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RA
     Finnerty J.R., Martindale M.Q.;
     "Homeoboxes in sea anemones (Cnidaria: Anthozoa): a PCR-based survey of
RT
     Nematostella vectensis and Metridium senile.";
RT
     Biol. Bull. 193:62-76(1997).
RL
     EMBL; U42727; AAA86626.1; -.
DR
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DR
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DR
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DT
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DT
DΕ
     CHv-Hbll protein (Fragment).
GN
     CHV-HB11.
OS
     Chaetopterus variopedatus.
     Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
OC
     Spionida; Chaetopteridae; Chaetopterus.
OC
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OX
RN
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     Irvine S.M., Warinner S.A., Hunter J.D., Martindale M.Q.;
RA
     "A survey of homeobox genes in Chaetopterus variopedatus and analysis
RT
     of polychaete homeodomains.";
RT
     Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
RL
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1 NQKKFIEKKD RDRISNEIGL DDRQIKY

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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DT
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DT
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DE
GN
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OS
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OC
     Rhizocephala; Kentrogonida; Sacculinidae; Sacculina.
OC
     NCBI TaxID=51650;
OX
RN
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RP
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     MEDLINE=98334561; PubMed=9667986;
RX
     Mouchel-Vielh E., Rigolot C., Gibert J.M., Deutsch J.S.;
RA
     "Molecules and the body plan: the Hox genes of Cirripedes
RT
RT
     (Crustacea).";
     Mol. Phylogenet. Evol. 9:382-389(1998).
RL
     EMBL; U79471; AAD00342.1; -.
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FT
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     01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DT
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DE
OS
     Beroe ovata.
     Eukaryota; Metazoa; Ctenophora; Cyclocoela; Beroida; Beroidae; Beroe.
OC
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RP
     Witchel H.J., Meech R.W.;
RA
     "BHox26 - Beroe Homeobox.";
RT
     Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
RL
     EMBL; U89381; AAB49471.1; -.
DR
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     InterPro; IPR001356; Homeobox.
DR
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     PRINTS; PR00024; HOMEOBOX.
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     ProDom; PD000010; Homeobox; 1.
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DT
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DT
     01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DT
     Homeobox protein BHox35 (Fragment).
DΕ
OS
     Beroe ovata.
     Eukaryota; Metazoa; Ctenophora; Cyclocoela; Beroida; Beroidae; Beroe.
OC
OX
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RA
     Witchel H.J., Meech R.W.;
     "BHox35 - Beroe Homeobox.";
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     Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
RL
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DR
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     InterPro; IPR001356; Homeobox.
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     01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
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DT
DE
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OS
     Artemia salina (Brine shrimp).
OC
     Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;
OC
     Artemiidae; Artemia.
OX
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RX
     MEDLINE=97338099; PubMed=9192646;
     Escriva H., Safi R., Hanni C., Langlois M.C., Saumitou-Laprade P.,
RA
RA
     Stehelin D., Capron A., Pierce R., Laudet V.;
RT
     "Ligand binding was acquired during evolution of nuclear receptors.";
RL
     Proc. Natl. Acad. Sci. U.S.A. 94:6803-6808(1997).
CC
     -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC
     -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
DR
     EMBL; U93418; AAC83395.1; -.
DR
     InterPro; IPR001628; Znf C4steroid.
DR
     Pfam; PF00105; zf-C4; 1.
DR
     ProDom; PD000035; Znf_C4steroid; 1.
DR
     SMART; SM00399; ZnF_C4; 1.
KW
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DT
     01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE
     CG12485 protein.
GN
     CG12485.
OS
     Drosophila melanogaster (Fruit fly).
OC
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OC
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     George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
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Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA
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RA
     de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA
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     Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
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     Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA
     Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA
RT
     "The genome sequence of Drosophila melanogaster.";
RL
     Science 287:2185-2195(2000).
     EMBL; AE003791; AAF57423.1; -.
DR
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DT
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DE
     Cysteine proteinase (Fragment).
OS
     Bombyx mori (Silk moth).
     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC
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OX
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RP
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RX
     MEDLINE=94086476; PubMed=8262908;
     Takahashi S.Y., Yamamoto Y., Shionoya Y., Kageyama T.;
RA
RT
     "Cysteine proteinase from the eggs of the silkmoth, Bombyx mori:
     identification of a latent enzyme and characterization of activation
RT
RT
     and proteolytic processing in vivo and in vitro.";
RL
     J. Biochem. 114:267-272(1993).
SQ
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DT
DT
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DE
     HOX OR MYX4.
GN
     Tetracapsula bryozoides.
OS
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RP
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RX
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RA
     Anderson C.L., Canning E.U., Okamura B.;
     "A triploblast origin for Myxozoa?";
RT
     Nature 392:346-347(1998).
RL
     EMBL; AJ005124; CAA06387.1; -.
DR
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DR
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KW
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GN
OS
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OC
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OC
OC
     Ephydroidea; Drosophilidae; Drosophila.
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OX
RN
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RP
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     MEDLINE=93281593; PubMed=8099440;
RX
RA
     Dear T.N., Sanchez-Garcia I., Rabbitts T.H.;
RT
     "The HOX11 gene encodes a DNA-binding nuclear transcription factor
RT
     belonging to a distinct family of homeobox genes.";
     Proc. Natl. Acad. Sci. U.S.A. 90:4431-4435(1993).
RL
DR
     EMBL; L08618; AAA28612.1; -.
DR
     FlyBase; FBgn0010394; Hox11-D125.
DR
     InterPro; IPR001356; Homeobox.
DR
     Pfam; PF00046; homeobox; 1.
DR
     ProDom; PD000010; Homeobox; 1.
FT
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                           1
                   27
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                          2.7
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SQ
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       1 LYQKYLSPAD RDEIAASLGL SNAQVIT
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                                     PRT;
                                             29 AA.
ID
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DT
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DT
     01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT
     01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE
     Von Willebrand factor (Fragment).
OS
     Pongo pygmaeus (Orangutan).
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
OC
     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
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     MEDLINE=20072937; PubMed=10603266;
RX
RA
     Chaves R., Sampaio I., Schneider M.P., Schneider H., Page S.L.,
RA
     Goodman M.;
RT
     "The place of Callimico goeldii in the Callitrichine phylogenetic
     tree: evidence from von Willebrand factor gene intron II sequences.";
RT
RL
     Mol. Phylogenet. Evol. 13:392-404(1999).
DR
     EMBL; AF092833; AAF77601.1; -.
FT
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FT
     NON TER
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SQ
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     029394;
DT
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DΤ
     01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DΤ
     01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE
     Growth hormone receptor (Fragment).
GN
     GHR.
OS
     Canis familiaris (Dog).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX
     NCBI TaxID=9615;
RN
RP
     SEQUENCE FROM N.A.
RX
     MEDLINE=97049323; PubMed=8894053;
RA
     Venta P.J., Brouillette J.A., Yuzbasiyan-Gurkan V., Brewer G.J.;
RТ
     "Gene-specific universal mammalian sequence-tagged sites: application
RТ
     to the canine genome.";
RT.
     Biochem. Genet. 34:321-341(1996).
DR
     EMBL; L77673; AAA97423.1; -.
KW
     Receptor.
FΤ
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FT
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                          23
SQ
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DT
     01-MAY-2000 (TrEMBLrel. 13, Created)
DT
     01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT
     01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE
     Vitronectin (Fragment).
     Canis familiaris (Dog).
OS
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX
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RN
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RP
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RX
     MEDLINE=92207982; PubMed=1372829;
RA
     Nakashima N., Miyazaki K., Ishikawa M., Yatohgo T., Ogawa H.,
RA
     Uchibori H., Matsumoto I., Seno N., Hayashi M.;
RT
     "Vitronectin diversity in evolution but uniformity in ligand binding
RT
     and size of the core polypeptide.";
RL
     Biochim. Biophys. Acta 1120:1-10(1992).
DR
     InterPro; IPR000886; ER target.
DR
     PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
FT
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                          1
     NON TER
FT
                  24
                         24
     SEQUENCE
                24 AA; 2745 MW; 94F0054986FE1215 CRC64;
SQ
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Q9TRS7 Length: 24 December 22, 2002 19:30 Type: P Check: 2610 ...
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## 1 AQESXKGRVT EGFNADRKOO ODEL

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DТ
     01-MAY-2000 (TrEMBLrel. 13, Created)
DT
     01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DТ
     01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
     Glutamate dehydrogenase isoform I (EC 1.4.1.2) (Fragment).
DF.
OS
     Bos taurus (Bovine).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC
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RN
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RX
     MEDLINE=96061967; PubMed=7588764;
RA
     Cho S.W., Lee J., Choi S.Y.;
RT
     "Two soluble forms of glutamate dehydrogenase isoproteins from bovine
RT
     brain.";
RL
     Eur. J. Biochem. 233:340-346(1995).
RN
     [2]
RP
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RX
     MEDLINE=96043916; PubMed=7581004;
RA
     Lee J., Kim S.W., Cho S.W.;
     "A novel glutamate dehydrogenase from bovine brain: purification and
RT
RT
     characterization.";
RL
     Biochem. Mol. Biol. Int. 36:1087-1096(1995).
SO
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AC
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חת
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DT
     01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE
     Glutamate dehydrogenase isoform II (EC 1.4.1.2) (Fragment).
OS
     Bos taurus (Bovine).
OC.
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC.
     Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC
     Bovidae; Bovinae; Bos.
OX
     NCBI TaxID=9913;
RN
     [1]
RP
     SEQUENCE.
     MEDLINE=96061967; PubMed=7588764;
RX
RA
     Cho S.W., Lee J., Choi S.Y.;
RT
     "Two soluble forms of glutamate dehydrogenase isoproteins from bovine
RT
     brain.";
RL
     Eur. J. Biochem. 233:340-346(1995).
SO
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       1 VEAAADREDD PNFFK
!!AA SEQUENCE 1.0
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AC
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     01-MAY-2000 (TrEMBLrel. 13, Created)
DT
     01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DТ
DT
DE
     VAMP/synaptobrevin-2 (Fragment).
OS
     Bos taurus (Bovine).
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
OC
     Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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Bovidae; Bovinae; Bos.
OC
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OX
RN
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RΡ
     MEDLINE=93374072; PubMed=8365494;
RX
     Horikawa H.P., Saisu H., Ishizuka T., Sekine Y., Tsugita A., Odani S.,
RA
     Abe T.;
RA
RT.
     FEBS Lett. 330:236-240(1993).
     InterPro; IPR001388; Synaptobrevin.
DR
     Pfam; PF00957; synaptobrevin; 1.
DR
DR
     ProDom; PD001229; Synaptobrevin; 1.
     PROSITE; PS00417; SYNAPTOBREVIN; 1.
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SO
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DΤ
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     01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DΨ
DT
     01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE
     ORF22.
     Pinus thunbergii (Green pine) (Japanese black pine).
OS
OG
     Chloroplast.
OC
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OC
     Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX
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RN
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RA
     Tsudzuki J., Nakashima K., Tsudzuki T., Hiratsuka J., Shibata M.,
RA
     Wakasugi T., Sugiura M.;
RT
     "Chloroplast DNA of black pine retains a residual inverted repeat
RT
     lacking rRNA genes: nucleotide sequences of trnQ, trnK, psbA, trnI and
RT
     trnH and the absence of rps16.";
RL
     Mol. Gen. Genet. 232:206-214(1992).
RN
     [2]
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RP
RX
     MEDLINE=95094312; PubMed=8001170;
RA
     Tsudzuki J., Ito S., Tsudzuki T., Wakasugi T., Sugiura M.;
RT
     "A new gene encoding tRNA(Pro) (GGG) is present in the chloroplast
     genome of black pine: a compilation of 32 tRNA genes from black pine
RТ
RТ
     chloroplasts.";
     Curr. Genet. 26:153-158(1994).
RL
RN
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RP
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RX
     MEDLINE=95024047; PubMed=7937893;
RA
     Wakasugi T., Tsudzuki J., Ito S., Nakashima K., Tsudzuki T.,
     Sugiura M.;
RA
RT
     "Loss of all ndh genes as determined by sequencing the entire
RT
     chloroplast genome of the black pine Pinus thunbergii.";
RT.
     Proc. Natl. Acad. Sci. U.S.A. 91:9794-9798(1994).
RN
     [4]
RP
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RA
     Sugiura M.;
RL
     Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
RN
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RP
RX
     MEDLINE=94138245; PubMed=8305874;
RA
     Li J., Goldschmidt-Clermont M., Timko M.;
RT
     "Chloroplast-encoded chlB is required for light-independent
RT
     protochlorophyllide reductase activity in Chlamydomonas reinhardtii.";
RT.
     Plant Cell 5:1817-1829(1993).
DR
     EMBL; D17510; BAA04307.1; -.
DR
     EMBL; D11467; BAA02023.1; -.
KW
     Chloroplast.
SQ
     SEQUENCE
                22 AA; 2606 MW; 0A95CB0443BCAEC5 CRC64;
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ΙD
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     01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DТ
     01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DТ
DF.
     Ribosomal protein S12 (Fragment).
GN
     RPS12.
     Abies alba (Edeltanne) (European silver fir).
OS
OG
     Mitochondrion.
     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC
OC
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OX
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RN
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RP
     Liepelt S.;
RA
RT
     "Sequence analysis of chosen regions of the mitochondrial genome of
RT
     Abies alba.";
RL
     Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR
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KW
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FT
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SQ
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DT
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DT
     01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT
     01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE
     Ribosomal protein S12 (Fragment).
     RPS12.
GN
     Pinus mugo.
OS
OG
     Mitochondrion.
OC
OC
     Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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RN
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RΡ
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RA
     Wachowiak W., Liepelt S., Prus-Glowacki W.;
RT
     "Sequence analysis of chosen regions of the mitochondrial genome of
RT
     Pinus mugo and P. sylvestris.";
RT.
     Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR
     EMBL; AF359576; AAK39117.1; -.
KW
     Mitochondrion.
FT
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                         23
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SO
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Q957T0 Length: 23 December 22, 2002 19:30 Type: P Check: 1370 ...
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Q957S8
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      01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DT
DT
DE
      Ribosomal protein S12 (Fragment).
GN
      RPS12.
OS
      Pinus sylvestris (Scots pine).
OG
      Mitochondrion.
OC
      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OC
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RN
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     Wachowiak W., Liepelt S., Prus-Glowacki W.;
     "Sequence analysis of chosen regions of the mitochondrial genome of
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     Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
RL
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FT
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DT
     01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE
     Acyl-(acyl-carrier-protein) hydrolase 33 kDa polypeptide, AH1
DE
     (EC 3.1.2.14) (Fragment).
     Cucurbita moschata (Cushaw squash) (Winter crookneck squash).
OS
OG
     Chloroplast.
OC
     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC
     Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC
     eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
OX
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RN
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RP
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RX
     MEDLINE=93004473; PubMed=1391766;
RA
     Imai H., Nishida I., Murata N.;
     "Acyl-(acyl-carrier protein) hydrolase from squash cotyledons specific
RТ
RT
     to long-chain fatty acids: purification and characterization.";
RT.
     Plant Mol. Biol. 20:199-206(1992).
SQ
     SEQUENCE
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 Q9T2K6 Length: 20 December 22, 2002 19:30 Type: P Check: 5922 ..
       1 GSSSLADRLX LGSLAXDGFS
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DT
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DT
     01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT
     01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE
     Chaperonin 21 (Fragment).
OS
     Spinacia oleracea (Spinach).
OG
     Chloroplast.
OC
     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC
     Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC
     Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX
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RN
     [1]
RΡ
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     MEDLINE=95394976; PubMed=7665625;
RX
     Ryan M.T., Naylor D.J., Hoogenraad N.J., Hoj P.B.;
RA
RL
     J. Biol. Chem. 270:22037-22043(1995).
SO
     SEQUENCE
                24 AA; 2642 MW; B797841E1005A51A CRC64;
Q9T2H3 Length: 24 December 22, 2002 19:30 Type: P Check: 2853 ..
       1 ATVVAPKYTS IKPTADRVLI KIKE
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ID
     Q37852
                 PRELIMINARY;
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AC
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01-NOV-1996 (TrEMBLrel. 01, Created)
DT
     01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT
     01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DT
     A protein (Fragment).
DΕ
     Bacteriophage R17.
OS
     Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC
     Levivirus.
OC
     NCBI_TaxID=12026;
OX
RN
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RP
RX
     MEDLINE=74125852; PubMed=4361645;
     Rensing U.F.E., Coulson A., Schoenmakers J.G.G.;
RA
     "A sequence of 54 nucleotides from the A-protein cistron of Coliphage-
RT
RТ
     R17 RNA.";
     Eur. J. Biochem. 41:431-438(1974).
RL
DR
     EMBL; M24814; AAA32177.1; -.
FT
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FT
     NON TER
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                         2217 MW;
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                                            28 AA.
ID
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AC
     Q42209;
     01-NOV-1996 (TrEMBLrel. 01, Created)
DΤ
DT
     01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
     01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DТ
     Ubiquitin conjugating enzyme UBC10 (Fragment).
DF.
     Arabidopsis thaliana (Mouse-ear cress).
٠OS
     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC
OC
     Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC
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OX
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RN
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RC
     STRAIN=CV. COLUMBIA; TISSUE=SEEDLING;
RA
     Desprez T., Amselem J., Chiapello H., Caboche M., Hofte H.;
RL
     Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
DR
     EMBL; Z29145; CAA82396.1; -.
DR
     HSSP; P15731; 1QCQ.
DR
     InterPro; IPR000608; UBQ conjugat.
DR
     Pfam; PF00179; UQ con; 1.
DR
     ProDom; PD000461; UBQ_conjugat; 1.
FT
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ΙD
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     01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT
     01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DT
DE
     Genomic DNA, chromosome 5, P1 clone: MVP2.
OS
     Arabidopsis thaliana (Mouse-ear cress).
OC
     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC
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OC
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OX
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RN
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RP
RC
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RA
     Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA
     Tabata S.;
RT
     "Structural analysis of Arabidopsis thaliana chromosome 5. XI.";
```

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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
RI.
     EMBL; AB025636; BAB11485.1;
DR
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DТ
     01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DΨ
     01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
DF.
     Catalase (Fragment).
OS
     Cucumis sativus (Cucumber).
     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC
     Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC
     eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OC
OX
     NCBI TaxID=3659;
RN
     [1]
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RΡ
RC
     TISSUE=COTYLEDON;
     MEDLINE=96104306; PubMed=8564304;
RX
     Toyama T., Teramoto H., Takeba G., Tsuji H.;
RA
     "Cytokinin induces a rapid decrease in the levels of mRNAs for
RT
     catalase, 3-hydroxy-3-methylglutaryl CoA reductase, lectin and other
RT
     unidentified proteins in etiolated cotyledons of cucumber.";
RT
     Plant Cell Physiol. 36:1349-1359(1995).
RL
     EMBL; D63385; BAA09701.1; -.
DR
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FT
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                23 AA;
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SQ
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DT
     01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT
     01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DT
     Chloroplast 50S ribosomal protein L18 beta (Fragment).
DΕ
     Spinacia oleracea (Spinach).
OS
     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC
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OC
     Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OC.
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     [1]
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RP
RC
     STRAIN=CV. ALWARO; TISSUE=LEAF;
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RX
     Yamaguchi K., Subramanian A.R.;
RA
     "The plastid ribosomal proteins. Identification of all the proteins in
RT
RT
     the 50 S subunit of an organelle ribosome (chloroplast).";
     J. Biol. Chem. 275:28466-28482(2000).
RL
     -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 5S RIBOSOMAL RNA.
CC
CC
     -!- SUBCELLULAR LOCATION: CHLOROPLAST.
     -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC
CC
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     -!- SIMILARITY: BELONGS TO THE L18P FAMILY OF RIBOSOMAL PROTEINS.
CC
KW
     Ribosomal protein; Chloroplast; rRNA-binding.
FT
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                  26
                         26
                26 AA;
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SQ
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 DT
      01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DT
      01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
      Chloroplast 50S ribosomal protein L18 alpha (Fragment).
 DE
OS
      Spinacia oleracea (Spinach).
OC
      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC
      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
      Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OC
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RN
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RA
      Yamaguchi K., Subramanian A.R.;
      "The plastid ribosomal proteins. Identification of all the proteins in
RT
RТ
     the 50 S subunit of an organelle ribosome (chloroplast).";
RL
     J. Biol. Chem. 275:28466-28482(2000).
CC
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CC
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CC
     -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 11.5 KDA.
CC
CC
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KW
FT
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                   29
                          29
SQ
     SEQUENCE
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DΤ
     01-OCT-2001 (TrEMBLrel. 18, Created)
DT
     01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
     01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DT
DE
     Thylakoid lumenal 25.3 kDa protein (Fragment).
     Spinacia oleracea (Spinach).
OS
OC
     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC
     Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC.
     Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
ΟX
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RN
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RC.
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RX
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RA
     Schubert M., Petersson U.A., Haas B.J., Funk C., Schroeder W.P.,
RΑ
     Kieselbach T.;
RT
     "Proteome map of the chloroplast lumen of Arabidopsis thaliana.";
RT.
     J. Biol. Chem. 277:8354-8365(2002).
CC
     -!- SUBCELLULAR LOCATION: CHLOROPLAST; WITHIN THE THYLAKOID LUMEN.
CC
     -!- MASS SPECTROMETRY: MW=25300; METHOD=MALDI.
KW
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FT
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                         19
SO
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 P83089 Length: 19 December 22, 2002 19:30 Type: P Check: 4307
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ID
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AC
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DT
     01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT
DT
     01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE
     CMETI-B=TRYPSIN inhibitor.
OS
     Cucumis melo (Muskmelon).
OC
     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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OC
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OX
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RN
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RX
RA
     Lee C.F., Lin J.Y.;
RT
     "Amino acid sequences of trypsin inhibitors from the melon Cucumis
RT
     melo.";
RL
     J. Biochem. 118:18-22(1995).
     HSSP; P12071; 2ETI.
DR
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     InterPro; IPR000737; Squash.
DR
     Pfam; PF00299; squash; 1.
DR
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     ProDom; PD003401; Squash; 1.
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SQ
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DΤ
     01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE
     23 kDa heat-induced protein (Fragment).
OS
     Lycopersicon esculentum (Tomato).
     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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     Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC.
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     MEDLINE=96351184; PubMed=8742333;
RA
     Sabehat A., Weiss D., Lurie S.;
RТ
     "The correlation between heat-shock protein accumulation and
RT
     persistence and chilling tolerance in tomato fruit.";
RT.
     Plant Physiol. 110:531-537(1996).
SO
     SEQUENCE
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                                  9B0D3F77BFEE6CE3 CRC64;
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DT
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DT
     01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT
     01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE
     TRANSFERRIN=PEPTIDE 21 (Fragment).
     Rattus sp.
OS
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
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RN
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RP
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RX
     MEDLINE=92165927; PubMed=1791188;
RA
     Cavanaugh P.G., Nicolson G.L.;
RT
     "Lung-derived growth factor that stimulates the growth of lung-
     metastasizing tumor cells: identification as transferrin.";
RT
     J. Cell. Biochem. 47:261-271(1991).
RT.
FT
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     NON TER
FT
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      01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DT
DE
      B230218P12Rik protein (Fragment).
GN
     B230218P12RIK.
     Mus musculus (Mouse).
OS
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
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RA
     Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
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RA
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RA
     Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA
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RA
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RA
     Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
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     Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
     Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA
RA
     Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
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     Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA
     Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA
     Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA
     Hayashizaki Y.;
RT
     "Functional annotation of a full-length mouse cDNA collection.";
RL
     Nature 409:685-690(2001).
     EMBL; AK021007; BAB32275.1; -.
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DT
     01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE
     2610020J05Rik protein (Fragment).
GN
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OS
     Mus musculus (Mouse).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC
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RA
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RA
     Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
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Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
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     Hayashizaki Y.;
RA
     "Functional annotation of a full-length mouse cDNA collection.";
RT
     Nature 409:685-690(2001).
RT.
     EMBL; AK019213; BAB31604.1; -.
DR
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DR
                  27
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FT
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                        3299 MW;
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TD
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AC
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     01-NOV-1996 (TrEMBLrel. 01, Created)
DT
     01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT
DT
     01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
     Hox3.5 homeobox homolog protein (Fragment).
DF.
OS
     Rattus norvegicus (Rat).
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
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OC
OX
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RN
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RP
RC
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RC
     MEDLINE=94271262; PubMed=7911662;
RX
     Iimura T., Oida S., Takeda K., Maruoka Y., Sasaki S.;
RA
     "Changes in homeobox-containing gene expression during ectopic bone
RT
     formation induced by bone morphogenetic protein.";
RT
     Biochem. Biophys. Res. Commun. 201:980-987(1994).
RL
     EMBL; S71286; AAB31006.1; -.
DR
     InterPro; IPR001356; Homeobox.
DR
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     Pfam; PF00046; homeobox; 1.
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     ProDom; PD000010; Homeobox; 1.
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NON_TER
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ID
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AC
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DT
     01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT
     01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DT
     Mszf76 (Fragment).
DΕ
GN
     MSZF76.
     Mus musculus (Mouse).
OS
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC
     NCBI TaxID=10090;
OX
RN
     [1]
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RP
RC
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     MEDLINE=98296253; PubMed=9630514;
RX
     Agata Y., Matsuda E., Shimizu A.;
RA
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RТ
     "Rapid and efficient cloning of cDNAs encoding Krueppel-like zinc
RT
     finger proteins by degenerate PCR.";
RL
     Gene 213:55-64(1998).
DR
     EMBL; AB010321; BAA31377.1; -.
DR
     InterPro; IPR000822; Znf C2H2.
DR
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DR
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DR
     SMART; SM00355; ZnF C2H2; 1.
DR
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DR
     PROSITE; PS50157; ZINC FINGER C2H2 2; 1.
KW
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FT
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FΤ
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SQ
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     Q9JIU0
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AC
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DΨ
     01-OCT-2000 (TrEMBLrel. 15, Created)
DТ
     01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT
     01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DF.
     Protocadherin-T5 (Fragment).
GN
     PCDH-T5.
OS
     Rattus norvegicus (Rat).
OC
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OC
     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX
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RA
     Johnson K.J., Patel S.R., Boekelheide K.;
RT
     "Multiple cadherin superfamily members with unique expression profiles
RT
     are produced in rat testis.";
RL
     Endocrinology 141:675-683(2000).
DR
     EMBL; AF177699; AAF87074.1; -.
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     01-MAY-2000 (TrEMBLrel. 13, Created)
DT
     01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT
     01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DT
DΕ
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     Mus musculus (Mouse).
OS
OC
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OC
OX
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RN
     [1]
RP
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RC
     STRAIN=129/SVJ; TISSUE=LIVER;
RX
     MEDLINE=20102720; PubMed=10636908;
RA
     Bergsdorf C., Paliga K., Kreger S., Masters C.L., Beyreuther K.;
RТ
     "Identification of cis-Elements Regulating Exon 15 Splicing of the
RT
     Amyloid Precursor Protein Pre-mRNA.";
RL
     J. Biol. Chem. 275:2046-2056(2000).
DR
     EMBL; AF199005; AAF20194.1; -.
DR
     EMBL; AF199003; AAF20194.1; JOINED.
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DR
      EMBL; AF199004; AAF20194.1; JOINED.
 FT
      NON TER
                    1
                           1
      NON TER
 FT
                   25
                          25
                 25 AA;
      SEQUENCE
 SQ
                         2608 MW; 276F026D582421D0 CRC64;
 Q9QX46 Length: 25 December 22, 2002 19:30 Type: P Check: 4770
        1 ENEVEPVDAR PAADRGLTTR PGSGL
 !!AA SEQUENCE 1.0
TD
     Q9ET00
                  PRELIMINARY;
                                    PRT;
                                             20 AA.
AC
     09ET00;
DT
     01-MAR-2001 (TrEMBLrel. 16, Created)
DT
     01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT
     01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DΕ
     EIF4H (Fragment).
os
     Mus musculus (Mouse).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX
     NCBI TaxID=10090;
RN
     [1]
RP
     SEQUENCE FROM N.A.
     STRAIN=129/SV;
RC.
RA
     Green E.D.;
     Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RL
DR
     EMBL; AF289665; AAF99335.1; -.
FT
     NON TER
                   20
                          20
SQ
     SEQUENCE
                 20 AA;
                         2188 MW;
                                  8AFFAC0FB953E8F5 CRC64;
 Q9ET00 Length: 20 December 22, 2002 19:30 Type: P Check: 5807
       1 MADFDTYDDR AYSSFGGGRG
!!AA SEQUENCE 1.0
     Q9Z1I5
                 PRELIMINARY;
                                    PRT;
                                            19 AA.
AC
     Q9Z1I5;
     01-MAY-1999 (TrEMBLrel. 10, Created)
DT
DT
     01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
     01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DT
     Calcineurin A alpha (EC 3.1.3.16) (Fragment).
DΕ
OS
     Rattus sp.
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC
OX
     NCBI TaxID=10118;
RN
     [1]
RP
     SEQUENCE FROM N.A.
     TISSUE=LIVER;
RC
RX
     MEDLINE=93111954; PubMed=1335233;
     Chang C., Takeda T., Mukai H., Shuntoh H., Kuno T., Tanaka C.;
RA
RT
     "Molecular cloning and characterization of the promoter region of the
RT
     calcineurin A alpha gene.";
RL
     Biochem. J. 288:801-805(1992).
DR
     EMBL; D10480; BAA01283.1; -.
KW
     Hydrolase.
FΨ
     NON TER
                  19
                         19
SQ
     SEQUENCE
                19 AA;
                        2115 MW; F905F8B134CCEC57 CRC64;
 Q9Z1I5 Length: 19 December 22, 2002 19:30 Type: P Check: 4927
       1 MSEPKAIDPK LSTTDRVVK
!!AA SEQUENCE 1.0
ID
     Q62256
                 PRELIMINARY;
                                    PRT;
                                            18 AA.
AC
     Q62256;
     01-NOV-1996 (TrEMBLrel. 01, Created)
     01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
     01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DT
DE
     Spermatogenic-specific proenkephalin.
GN
     PENK-RS.
OS
     Mus musculus (Mouse).
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC
     NCBI TaxID=10090;
OX
RN
     [1]
     SEQUENCE FROM N.A.
RP
     MEDLINE=90287163; PubMed=2355920;
RX
     Kilpatrick D.L., Zinn S.A., Fitzgerald M., Higuchi H., Sabol S.L.,
RA
     Meyerhardt J.;
RA
     "Transcription of the rat and mouse proenkephalin genes is initiated
RT
     at distinct sites in spermatogenic and somatic cells.";
RT
RL
     Mol. Cell. Biol. 10:3717-3726(1990).
     EMBL; M55181; AAA40127.1; -.
DR
     MGD; MGI:104628; Penk-rs.
DR
SO
     SEOUENCE
               18 AA; 2043 MW; B96E10CC7049FA76 CRC64;
Q62256 Length: 18 December 22, 2002 19:30 Type: P Check: 3193
       1 MSSGKQDSPW EDRIPPGR
!!AA SEQUENCE 1.0
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                 PRELIMINARY;
                                    PRT;
                                            25 AA.
ΙD
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AC
DT
     01-NOV-1996 (TrEMBLrel. 01, Created)
DT
     01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT
     01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE
     Hox1.8 homeobox homolog protein (Fragment).
OS
     Rattus sp.
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX
     NCBI_TaxID=10118;
RN
     [1]
     SEQUENCE FROM N.A.
RP
RX
     MEDLINE=94271262; PubMed=7911662;
RA
     Iimura T., Oida S., Takeda K., Maruoka Y., Sasaki S.;
RT
     "Changes in homeobox-containing gene expression during ectopic bone
     formation induced by bone morphogenetic protein.";
RT
     Biochem. Biophys. Res. Commun. 201:980-987(1994).
RL
     EMBL; S71275; AAB31001.1; -.
DR
     InterPro; IPR001356; Homeobox.
DR
DR
     Pfam; PF00046; homeobox; 1.
     ProDom; PD000010; Homeobox; 1.
DR
KW
     DNA-binding; Homeobox; Nuclear protein.
     NON TER
FT
                   1
                          1
     SEQUENCE
                25 AA; 3134 MW; C54E951607BD27B1 CRC64;
SO
Q63985 Length: 25 December 22, 2002 19:30 Type: P Check: 5721 ..
       1 LFNMYLTRER RLEISRSVHL TDRQV
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     Q61159
                                    PRT;
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ID
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     Q61159;
AC
     01-NOV-1996 (TrEMBLrel. 01, Created)
DT
     01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT
     01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DT
DE
     NN8-AG (Fragment).
GN
     RRG1 OR NN8-AG.
     Mus musculus (Mouse).
OS
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC
OX
     NCBI TaxID=10090;
RN
     [1]
     SEQUENCE FROM N.A.
RP
RC
     STRAIN=129SV;
     MEDLINE=96315660; PubMed=8754834;
RX
RA
     Shago M., Giguere V.;
RT
     "Isolation of a novel retinoic acid-responsive gene by selection of
RT
     genomic fragments derived from CpG-island-enriched DNA.";
RL
     Mol. Cell. Biol. 16:4337-4348(1996).
DR
     EMBL; U50384; AAB38132.1; -.
DR
     MGD; MGI:108048; Rrg1.
                         32
FT
     NON TER
                  32
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32 AA; 3470 MW; 9571FBD80B1FCA84 CRC64;
SO
     SEQUENCE
  O61159 Length: 32 December 22, 2002 19:30 Type: P Check: 837
       1 MAASMCDVFS FCVGVADRAR GSVEVRYVDS IK
!!AA SEQUENCE 1.0
     Q923H1
                 PRELIMINARY;
                                    PRT;
                                            40 AA.
ID
AC
     Q923H1;
     01-DEC-2001 (TrEMBLrel. 19, Created)
DΤ
DТ
     01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
     01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DТ
     Aristaless-related homeobox protein Arx (Fragment).
DE
OS
     Cricetulus griseus (Chinese hamster).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
     Cricetulus.
OC
OX
     NCBI TaxID=10029;
RN
     [1]
RP
     SEQUENCE FROM N.A.
RA
     Ohira R.H., Zhang Y.H., Guo W., Dipple K., Shih S., Doerr J.,
RA
     Huang B.-L., Fu L., Abu-Khalil A., Geschwind D., McCabe E.;
     "Human ARX gene: genomic characterization and expression.";
RT
RL
     Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
     EMBL; AY038070; AAK93900.1; -.
DR
KW
     DNA-binding; Homeobox; Nuclear protein.
FT
     NON TER
                   1
                          1
     NON TER
                  40
                         40
FT
SQ
     SEQUENCE
                40 AA;
                        3815 MW;
                                  87A852768DB0CB6E CRC64;
Q923H1 Length: 40 December 22, 2002 19:30 Type: P Check: 2032
       1 PTPAVEGAVA SGALADPATA AADRRASSIA AXGSRPRSMP
!!AA SEQUENCE 1.0
     Q99KX5
                 PRELIMINARY;
                                    PRT:
                                            27 AA.
TD
AC
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     01-JUN-2001 (TrEMBLrel. 17, Created)
DT
DT
     01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT
     01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE
     Hypothetical 2.8 kDa protein.
OS
     Mus musculus (Mouse).
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OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX
     NCBI_TaxID=10090;
RN
     [1]
     SEQUENCE FROM N.A.
RP
RA
     Strausberg R.;
RL
     Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR
     EMBL; BC003968; AAH03968.1; -.
KW
     Hypothetical protein.
SQ
     SEQUENCE
                27 AA; 2832 MW;
                                  4008F368AF868B63 CRC64;
Q99KX5 Length: 27 December 22, 2002 19:30 Type: P Check: 9106 ...
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## 1 MASLPVVGSQ VPADRGYLGP RPAVQEH

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ID
AC
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     01-MAY-2000 (TrEMBLrel. 13, Created)
DT
DT
     01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT
     01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE
     Vitronectin (Fragment).
OS
     Cavia (guinea pigs).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae.
     NCBI_TaxID=10140;
OX
RN
     [1]
RΡ
     SEQUENCE.
RX
     MEDLINE=92207982; PubMed=1372829;
```

```
Nakashima N., Miyazaki K., Ishikawa M., Yatohgo T., Ogawa H.,
RA
     Uchibori H., Matsumoto I., Seno N., Hayashi M.;
RA
     "Vitronectin diversity in evolution but uniformity in ligand binding
RT
     and size of the core polypeptide.";
RT
     Biochim. Biophys. Acta 1120:1-10(1992).
RL
FT
     NON TER
                          1
                   1
     NON TER
                  24
                         24
FT
                24 AA;
                        2736 MW;
                                  OCD91505B6F22D0A CRC64;
     SEQUENCE
SO
Q9QVD0 Length: 24 December 22, 2002 19:30 Type: P Check: 3385
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                 PRELIMINARY;
                                    PRT;
                                            32 AA.
ID
     090V89
     Q9QV89;
AC
     01-MAY-2000 (TrEMBLrel. 13, Created)
DΤ
     01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT
DT
     01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
     SLP-14=FATTY acid-binding protein (Fragment).
DF.
OS
     Rattus sp.
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC
OX
     NCBI TaxID=10118;
RN
     [1]
     SEOUENCE.
RP
RX
     MEDLINE=93191717; PubMed=8447836;
RA
     Bansal M.P., Medina D.;
RT
     "Expression of fatty acid-binding proteins in the developing mouse
RT
     mammary gland.";
RL
     Biochem. Biophys. Res. Commun. 191:61-69(1993).
DR
     HSSP; P05413; 1HMT.
     InterPro; IPR000566; Lipocln cytFABP.
DR
DR
     Pfam; PF00061; lipocalin; 1.
FT
     NON TER
                   1
                          1
     NON TER
                  32
                          32
FT
                        3495 MW;
                                   67D23A0146E46AFE CRC64;
SO
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                32 AA;
 Q9QV89 Length: 32 December 22, 2002 19:30 Type: P Check: 581
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                                    PRT;
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ID
AC.
     Q9QV71;
     01-MAY-2000 (TrEMBLrel. 13, Created)
DT
DΤ
     01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT
     01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE
     Lactase-phlorizin hydrolase (Fragment).
OS
     Rattus sp.
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX
     NCBI TaxID=10118;
RN
     [1]
RΡ
     SEQUENCE.
RX
     MEDLINE=93293888; PubMed=8514793;
RA
     Dudley M.A., Hachey D.L., Quaroni A., Hutchens T.W., Nichols B.L.,
RA
     Rosenberger J., Perkinson J.S., Cook G., Reeds P.J.;
     "In vivo sucrase-isomaltase and lactase-phlorizin hydrolase turnover
RТ
RT
     in the fed adult rat.";
     J. Biol. Chem. 268:13609-13616(1993).
RT.
                17 AA; 1947 MW; 08941FD316F9692F CRC64;
SQ
     SEQUENCE
Q9QV71 Length: 17 December 22, 2002 19:30 Type: P Check: 1363 ...
       1 DWEDRNFIAA GPLTNDL
!!AA_SEQUENCE 1.0
ID
     Q61461
                 PRELIMINARY;
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AC
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DT
     01-NOV-1996 (TrEMBLrel. 01, Created)
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01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
DT
     01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DT
     Cytochrome P-450b (Phenobarbital-inducible) (Fragment).
DE
GN
     CYP2B13.
     Mus musculus (Mouse).
OS
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC
OX
     NCBI TaxID=10090;
RN
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RP
RX
     MEDLINE=84207435; PubMed=6547088;
     Stupans I., Ikeda T., Kessler D.J., Nebert D.W.;
RΑ
     "Characterization of a cDNA clone for mouse phenobarbital-inducible
RТ
RТ
     cytochrome P-450b.";
     DNA 3:129-137(1984).
RL
CC
     -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
     EMBL; K02409; AAA37510.1; -.
DR
     MGD; MGI:88599; Cyp2b13.
DR
DR
     InterPro; IPR001128; Cytochrome_P450.
     Pfam; PF00067; p450; 1.
DR
KW
     Heme; Monooxygenase; Oxidoreductase.
FT
     NON TER
                   1
                          1
                  25
FT
     NON TER
                         25
SQ
     SEQUENCE
                25 AA;
                        2979 MW; B9DFF7A57355A1B0 CRC64;
Q61461 Length: 25 December 22, 2002 19:30 Type: P Check: 4925
       1 SHRLPTLDDR SKMPYTDAVI HEIQR
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                                    PRT;
                                            19 AA.
ID
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AC
     01-NOV-1996 (TrEMBLrel. 01, Created)
DΤ
DΤ
     01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
ΤП
     01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DΕ
     Outer coat protein (VP2) (Fragment).
OS
     Bluetonque virus.
     Viruses; dsRNA viruses; Reoviridae; Orbivirus.
OC
OX
     NCBI TaxID=12591;
RN
     [1]
RP
     SEQUENCE FROM N.A.
RX
     MEDLINE=88265863; PubMed=2838961;
RA
     Gould A.R., Hyatt A.D., Eaton B.T.;
RT
     "Morphogenesis of a bluetongue virus variant with an amino acid
RT
     alteration at a neutralization site in the outer coat protein, VP2.";
RL
     Virology 165:23-32(1988).
DR
     EMBL; M21355; AAA42845.1; -.
DR
     InterPro; IPR001742; Orbi VP2.
DR
     Pfam; PF00898; Orbi VP2; 1.
KW
     Coat protein.
FT
     NON TER
                   1
                          1
     NON TER
FT
                  19
                         19
                19 AA; 2608 MW; F0428841265D3061 CRC64;
SQ
     SEQUENCE
Q65747 Length: 19 December 22, 2002 19:30 Type: P Check: 4484 ..
       1 ERLKIFEHRN QRRDEDRFY
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ID
     066538
                 PRELIMINARY;
                                    PRT;
                                            35 AA.
AC
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     01-NOV-1996 (TrEMBLrel. 01, Created)
DT
     01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DТ
DΨ
     01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE
     3' proximal protein (Fragment).
OS
     Ebola virus.
     Viruses; ssRNA negative-strand viruses; Mononegavirales; Filoviridae;
OC
OC
     Ebola-like viruses.
OX
     NCBI_TaxID=11268;
RN
     [1]
RP
     SEQUENCE FROM N.A.
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```
MEDLINE=86124724; PubMed=3946083;
RX
     Kiley M.P., Wilusz J., McCormick J.B., Keene J.D.;
RA
RT
     "Conservation of the 3' terminal nucleotide sequences of Ebola and
RT
     Marburg virus.";
RL
     Virology 149:251-254(1986).
DR
     EMBL; M33062; AAA42976.1; -.
FT
     NON TER
                  35
                         35
SQ
     SEQUENCE
                35 AA;
                        4142 MW;
                                   F7778E5FC6283092 CRC64;
Q66538 Length: 35 December 22, 2002 19:30 Type: P Check: 8137
       1 MRKINNFLSL KFDDRNLKLK LLICNHTVDS EPHTS
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                                    PRT;
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ID
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DT
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     01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT
DT
     01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE
     Hypothetical 1.1 kDa protein (Fragment).
OS
     Murray valley encephalitis virus.
     Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC
OC
     Flavivirus.
OX
     NCBI_TaxID=11079;
RN
     [1]
RP
     SEQUENCE FROM N.A.
RX
     MEDLINE=88118912; PubMed=2828633;
     Hahn C.S., Hahn Y.S., Rice C.M., Lee E., Dalgarno L., Strauss E.G.,
RA
RA
     Strauss J.H.;
     "Conserved elements in the 3' untranslated region of flavivirus RNAs
RT
     and potential cyclization sequences.";
RT
     J. Mol. Biol. 198:33-41(1987).
RL
     EMBL; M35172; AAA66627.1; -.
DR
KW
     Hypothetical protein.
     NON TER
FΨ
                   1
                9 AA; 1055 MW; FF36D40AAB05A2C1 CRC64;
SQ
     SEQUENCE
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ΙD
                                    PRT;
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AC
DΤ
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DT
     01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT
     01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE
     X protein (Fragment).
OS
     Bovine papillomavirus.
OC
     Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC
     Papillomavirus.
OX
     NCBI TaxID=10571;
RN
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RP
     SEQUENCE FROM N.A.
RX
     MEDLINE=89067912; PubMed=2848926;
     Stamps A.C., Campo M.S.;
RA
RT
     "Mapping of two novel transcripts of Bovine papillomavirus type 4.";
RL
     J. Gen. Virol. 69:3033-3045(1988).
DR
     EMBL; M35264; AAA46926.1; -.
FT
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FT
     NON TER
                  22
                         22
SQ
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                        2273 MW;
                                  2801BC23480C9CF9 CRC64;
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       1 NAGPKPGTTP EDVADRPPDL PE
!!AA SEQUENCE 1.0
ID
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                                            39 AA.
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AC.
     Q9PWC1;
DT
     01-MAY-2000 (TrEMBLrel. 13, Created)
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DT
      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT
      01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DΕ
      P55-related MAGUK protein DLG3 (Fragment).
 GN
      DLG3.
 OS
      Brachydanio rerio (Zebrafish) (Zebra danio).
 OC
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC
      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC
      Cyprinidae; Danio.
 OX
      NCBI_TaxID=7955;
 RN
      [1]
RP
      SEQUENCE FROM N.A.
      Koenig C., Yan Y.L., Postlethwait J., Wendler S., Campos-Ortega J.A.;
RA
      "A recessive mutation leading to vertebral ankylosis is associated
RT
      with amino acid exchanges in the zebrafish homologue of the human
RT
      membrane associated guanylate kinase protein DLG3.";
RT
RL
      Mech. Dev. 84:1-12(1999).
DR
      EMBL; AF124436; AAD39393.1; -.
      InterPro; IPR004172; L27.
DR
DR
      Pfam; PF02828; L27; 1.
FT
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DΤ
     01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DF.
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GN
     LBX1.
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OS
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OX
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RN
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RA
     Dietrich S., Schubert F.R., Healy C., Sharpe P.T., Lumsden A.;
RТ
     "Specification of the hypaxial musculature.";
RL
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RN
     [2]
RP
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RA
     Schubert F.R., Dietrich S., Chapman S.C., Lumsden A.;
RT
     "Expression of the Lbx1 gene in the chick embryo.";
RL
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DR
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     01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT
     01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DT
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OS
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OC
OC
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Cyprinidae; Carassius.
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      Levine E.M., Schechter N.;
RT
      "Homeobox genes are expressed in the retina and brain of adult
RT
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RL
      Proc. Natl. Acad. Sci. U.S.A. 90:2729-2733(1993).
DR
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     01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT
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DE
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OS
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     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
OC.
     Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC.
     Cyprinidae; Carassius.
OX
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RT
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RL
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AC
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DΤ
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DT
     01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DT
DE
     Homeodomain (Fragment).
GN
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OS
     Petromyzon marinus (Sea lamprey).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
     Petromyzontiformes; Petromyzontidae; Petromyzon.
OC
OX
     NCBI TaxID=7757;
RN
     [1]
RP
     SEQUENCE FROM N.A.
RX
     MEDLINE=93317669; PubMed=8101001;
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OC

```
Pendleton J.W., Nagai B.K., Murtha M.T., Ruddle F.H.;
RA
RT
      "Expansion of the Hox gene family and the evolution of chordates.";
      Proc. Natl. Acad. Sci. U.S.A. 90:6300-6304(1993).
RL
DR
     EMBL; L14895; AAA02530.1; -.
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     PRINTS; PR00024; HOMEOBOX.
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     01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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DΕ
GN
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OS
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OC
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OC
OX
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RN
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     Pendleton J.W., Nagai B.K., Murtha M.T., Ruddle F.H.;
RA
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RT
RL
     Proc. Natl. Acad. Sci. U.S.A. 90:6300-6304(1993).
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DR
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     01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT
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DΕ
     Hox C10 (Fragment).
     Gallus gallus (Chicken).
OS
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
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     MEDLINE=98141813; PubMed=9473273;
RA
     Peale F.V. Jr., Mason K., Hunter A.W., Bothwell M.;
RT
     "Multiplex display polymerase chain reaction amplifies and resolves
RT
     related sequences sharing a single moderately conserved domain.";
     Anal. Biochem. 256:158-168(1998).
RL
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     01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT
     01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DT
     Phospholemman (FXYD domain-containing ion transport regulator 1)
DE
DE
     (Fragment).
OS
     Lamna nasus.
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC
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OC
OX
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RN
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RP
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RC
     TISSUE=RECTAL GLAND;
RA
     Schuurmans Stekhoven F.M.A.H., Flik G., Wendelaar Bonga S.E.;
RТ
     "Phospholemman in the rectal gland of sharks.";
RL
     Submitted (JUN-2001) to the SWISS-PROT data bank.
CC
     -!- FUNCTION: INDUCES A HYPERPOLARIZATION-ACTIVATED CHLORIDE CURRENT
CC
CC
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CC
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CC
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CC
     -!- PTM: MAJOR PLASMA MEMBRANE SUBSTRATE FOR CAMP-DEPENDENT PROTEIN
CC
         KINASE (PK-A) AND PROTEIN KINASE C (PK-C) IN SEVERAL DIFFERENT
CC
         TISSUES. PHOSPHORYLATED IN RESPONSE TO INSULIN AND ADRENERGIC
CC
         STIMULATION (BY SIMILARITY).
CC
     -!- SIMILARITY: BELONGS TO THE FXYD FAMILY.
DR
     InterPro; IPR000272; ATP1G1 PLM MAT8.
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- WHEN EXPRESSED IN XENOPUS OOCYTES. MAY HAVE A FUNCTIONAL ROLE IN
- DR PROSITE; PS01310; FXYD; PARTIAL.
- KW Transmembrane; Phosphorylation; Ionic channel; Ion transport;
- KW Microsome.
- FTNON TER 13 13
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DΤ
     01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DΤ
     01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DΕ
     Phospholemman (FXYD domain-containing ion transport regulator 1)
DF.
     (Fragment).
OS
     Triakis scyllium (Leopard shark) (Triakis scyllia).
OC.
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
     Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes; Triakidae;
OC.
OC
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OX
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RC
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RT
     "Phospholemman in the rectal gland of sharks.";
     Submitted (JUN-2001) to the SWISS-PROT data bank.
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- -!- FUNCTION: INDUCES A HYPERPOLARIZATION-ACTIVATED CHLORIDE CURRENT CC WHEN EXPRESSED IN XENOPUS OOCYTES. MAY HAVE A FUNCTIONAL ROLE IN CC CC MUSCLE CONTRACTION. CC
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- CC -!- PTM: MAJOR PLASMA MEMBRANE SUBSTRATE FOR CAMP-DEPENDENT PROTEIN CC KINASE (PK-A) AND PROTEIN KINASE C (PK-C) IN SEVERAL DIFFERENT CC TISSUES. PHOSPHORYLATED IN RESPONSE TO INSULIN AND ADRENERGIC

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CC
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     -!- SIMILARITY: BELONGS TO THE FXYD FAMILY.
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DT
     01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DΕ
     HoxClla (Fragment).
GN
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OS
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OC
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OC
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OX
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RN
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RP
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RA
     Kurosawa G., Yamada K., Ishiguro H., Hori H.;
RT
     "isolation of BAC Clones That Cover Seven Hox Clusters in Medaka
RТ
     Genome.";
RT.
     Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR
     EMBL; AB055740; BAB62853.1; -.
DR
     InterPro; IPR001356; Homeobox.
DR
     Pfam; PF00046; homeobox; 1.
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     ProDom; PD000010; Homeobox; 1.
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DT
     01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DΕ
     PO GLYCOPROTEIN=MYELIN major structural protein (Fragment).
OS
     Rana catesbeiana (Bull frog).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX
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RA
     Karthigasan J., Bauer T.K., Teplow D.B., Saavedra R.A.,
     Kirschner D.A.;
RA
     "Phylogenetically conserved amino acids of MBP and PO from amphibian
RT
RT
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     J. Mol. Neurosci. 3:185-188(1992).
RL
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FT
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SO
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1 IEVYTDREIQ SNVGSKVHLY

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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Nonmuscle alpha-action
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חת
ידת
DT
DE
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OS
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OC
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OC
OC.
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OX
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     MEDLINE=93100311; PubMed=1334489;
     Imamura M., Masaki T.;
RA
     "A novel nonmuscle alpha-actinin. Purification and characterization of
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RT
     J. Biol. Chem. 267:25927-25933(1992).
RL
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FT
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     01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT
     01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DT
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DE
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OS
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OX
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RN
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RP
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     MEDLINE=95050502; PubMed=7961672;
RX
     Solca F.F., Lurie D.I., Diltz C.D., Johnson R.S., Kumar S.,
RA
     Rubel E.W., Fischer E.H.;
RA
      "Identification and purification of a chicken brain neuroglia-
RT
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RT
      J. Biol. Chem. 269:27559-27565(1994).
RL
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        1 DGGEDRDAAV EEAVLGTGGC RTPK
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АC
      01-MAR-2001 (TrEMBLrel. 16, Created)
DT
      01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT
      01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DT
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DΕ
GN
      Human immunodeficiency virus type 1.
OS
      Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC
OX
      NCBI TaxID=11676;
RN
      [1]
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RP
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RC
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      Motomura K., Kusagawa S., Kato K., Nohtomi K., Lwin H.H., Tun K.M.,
RA
      Thwe M., Oo K.Y., Lwin S., Kyaw O., Zaw M., Nagai Y., Takebe Y.;
RA
RT
      "Emergence of new forms of human immunodeficiency virus type 1
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	•	
		;; ;

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RT
      intersubtype recombinants in central myanmar.";
RL
     AIDS Res. Hum. Retroviruses 16:1831-1843(2000).
DR
     EMBL; AB043899; BAB19213.1; -.
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     01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT
DΤ
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DΕ
     Tat protein (Fragment).
GN
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OS
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OC
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RA
     Gao F., Yue L., Craig S., Thornton C.L., Robertson D.L.,
RA
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RT
     "Genetic variation of HIV type 1 in four World Health Organization-
RT
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     (glycoprotein 160) clones representative of sequence subtypes A, B, C,
RT
RT
     and E. WHO Network for HIV Isolation and Characterization.";
RL
     AIDS Res. Hum. Retroviruses 10:1359-1368(1994).
RN
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RP
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RC
     STRAIN=020;
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     MEDLINE=96190564; PubMed=8627686;
     Gao F., Morrison S.G., Robertson D.L., Thornton C.L., Craig S.,
Karlsson G., Sodroski J., Morgado M., Galvao-Castro B.,
RA
RA
RA
     von Briesen H., Beddows S., Weber J., Sharp P.M., Shaw G.M.,
RA
     Hahn B.H.;
     "Molecular cloning and analysis of functional envelope genes from
RT
RT
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RT
     WHO and NIAID Networks for HIV Isolation and Characterization.";
RL
     J. Virol. 70:1651-1657(1996).
RN
RP
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RC
     STRAIN=020;
RA
     Allen E.E.;
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     Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
DR
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FT
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                 9 AA; 1098 MW; 5B76D40AB1AB01A3 CRC64;
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     01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DT
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DE
     Hypothetical protein HP0917.
GN
     HP0917.
OS
     Helicobacter pylori (Campylobacter pylori).
OC
     Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC
     Helicobacter.
OX
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      Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
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      Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
 RA
      Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
      Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
 RA
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      Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
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      Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
 RA
 RA
      Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
 RA
      Venter J.C.;
      "The complete genome sequence of the gastric pathogen Helicobacter
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RT
      pylori.";
RL
      Nature 388:539-547(1997).
DR
      EMBL; AE000601; AAD07968.1; -.
DR
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KW
SQ
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DΤ
     01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE
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GN
     RV3599C OR MTCY07H7B.23.
OS
     Mycobacterium tuberculosis.
     Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC
OC
     Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX
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RN
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     Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
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RΆ
     Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
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     Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA
     Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA
     Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA
     Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA
     Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT
     "Deciphering the biology of Mycobacterium tuberculosis from the
RT
     complete genome sequence.";
RL
     Nature 393:537-544(1998).
DR
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DR
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KW
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DE
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GN
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OS
     Vibrio cholerae.
     Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OC
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RN

[1]

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OX
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      [1]
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      Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
      Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
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      Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
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      Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
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      Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA
RA
      Fraser C.M.;
      "DNA sequence of both chromosomes of the cholera pathogen Vibrio
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RT
      cholerae.";
RL
      Nature 406:477-483(2000).
      EMBL; AE004159; AAF93900.1; -.
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     01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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GN
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OS
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OC
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OX
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RN
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RA
     Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RΑ
     Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RΑ
     McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
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     Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
     Fraser C.M.;
RA
RT
     "DNA sequence of both chromosomes of the cholera pathogen Vibrio
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RL
     Nature 406:477-483(2000).
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     01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT
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DΤ
DF.
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GN
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OS
     Escherichia coli 0157:H7.
     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC
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     Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA
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     Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA
     Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA
RA
     Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
     Welch R.A., Blattner F.R.;
RA
     "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RT
     Nature 409:529-533(2001).
RL
     EMBL; AE005252; AAG55068.1; -.
DR
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DT
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DT
DE
     Hypothetical protein MT3536.
GN
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OS
     Mycobacterium tuberculosis.
OC
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     Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
     Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
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RA
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RT
     "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT
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     Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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DR
KW
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     01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
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OS
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OX
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RA
     Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA
     Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA
RA
     Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
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Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.; "Genome sequence of Halobacterium species NRC-1."; RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000). DR EMBL; AE005097; AAG20207.1; -. KW Complete proteome. SQ SEQUENCE 32 AA; 3719 MW; D0F9677E650A578A CRC64;
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Q9HNL3 Length: 32 December 22, 2002 19:30 Type: P Check: 9872 ..

1 MVRVPVTDAG RAEMRERADR LETTAAFWRL VD

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